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R-HEMBA1001463

R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:  
66//Hs.36232:D80008

R-HEMBA1001478

R-HEMBA1001497

R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426

R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9  
e-79:528:84//Hs.23094:M19503

R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269

R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA702493

R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723

R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270

R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348

R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs  
.155464:AF088219

R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259  
:62//Hs.2229:X82324

R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:4  
56:77//Hs.159275:AF030880

R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030

R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652

R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63/  
/Hs.146395:AB002329

R-HEMBA1001589

R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-  
71:431:88//Hs.26625:W25874

R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
1.3e-73:533:82//Hs.103948:K00627

R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHA



SE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530  
 R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:  
 362:60//Hs.132206:AF039694  
 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158  
 R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-8  
 6:442:95//Hs.63888:AA203398  
 R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554  
 R-HEMBA1001658  
 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds  
 //1.3e-16:427:61//Hs.106511:AF029343  
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA  
 , complete cds//1.4e-93:493:92//Hs.107254:AC005943  
 R-HEMBA1001675  
 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA  
 A, complete cds//4.2e-103:534:94//Hs.7381:AF038962  
 R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424  
 R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916  
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.  
 3e-98:483:96//Hs.31720:AB014598  
 R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960  
 R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095  
 R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL  
 PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452  
 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs  
 .155464:AF088219  
 R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CO  
 NTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisi  
 ae]//7.1e-88:431:96//Hs.29203:AI344105

R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712  
R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:  
77//Hs.153014:AB002353  
R-HEMBA1001744  
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623  
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162  
R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145  
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306  
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721  
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053  
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243  
R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823  
R-nnnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180  
:AF039019  
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0500//9.0e-114:548:98//Hs.118164:AB007969  
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334  
R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF06  
8179  
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07  
290  
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707  
R-nnnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578  
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:14  
7:97//Hs.23476:AA401210  
R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250  
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513  
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446  
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.

1e-109:553:96//Hs.78946:AB014517  
R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853  
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative product  
s} //1.9e-37:357:76//Hs.53217:Z48051  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2  
[H.sapiens] //2.3e-32:193:94//Hs.9489:R84329  
R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.  
66710:X96969  
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128  
R-HEMBA1001910  
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens] //1.5e-73:347:100//Hs.30991:AA994438  
R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces ce  
revisiae] //5.1e-57:320:91//Hs.91251:U66685  
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706  
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125  
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kina  
se mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145  
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens] //2.9e-99:482:98//Hs.96849:AA879470  
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:8  
2//Hs.40100:AB002390  
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668  
R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452  
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866  
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421  
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048  
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825  
R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.

2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso  
log of a Rat gene) and a novel alternatively spliced gene. Contains a pu  
tative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178  
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932  
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717  
R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:  
88//Hs.153014:AB002353  
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6  
e-91:448:97//Hs.5687:AJ005801  
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930  
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837  
R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//  
Hs.1189:D38550  
R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538  
R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:6  
4//Hs.101238:Y11312  
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.  
4e-51:254:85//Hs.15731:AB011135  
R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764  
R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996  
R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354  
R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124  
:AF019369  
R-HEMBA1002113//Prostaglandin I2 (prostacyclin) synthase //1.4e-76:280:9  
0//Hs.61333:D83402  
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e  
-87:362:94//Hs.103443:AF065854  
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:9  
4:100//Hs.107747:AI357868

R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X8395

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R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734

R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199

R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642

R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337

R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674

R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915

R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043

R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081

R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457

R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622

R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958

R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357

R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503

R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342

R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315

R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151

R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606

R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814

R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202

R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426

R-HEMBA1002257

R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN  
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:  
W72675

R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314

R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595

R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818

R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679

R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8  
e-130:642:96//Hs.6162:AB018314

R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822

R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094

R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mR  
NA, complete cds//3.9e-123:661:93//Hs.119023:AF092563

R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435

R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237

R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:9  
1//Hs.25527:AC005954

R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-8  
7:429:96//Hs.13209:AI417849

R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267

R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:8  
0//Hs.74554:D38522

R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069

R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085

R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395

R-nnnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:48  
8:95//Hs.108115:AA582193

R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80/

/Hs.43681:AL022394  
R-HEMBA1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs  
.155464:AF088219  
R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995  
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133  
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449  
R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990  
R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972  
R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715  
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923  
R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700  
R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804  
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881  
R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012  
R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs  
.32567:AF073519  
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs  
.155464:AF088219  
R-xxxxxxxxxxxx//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:AF075587  
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904  
R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838  
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055  
R-HEMBA1002621  
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351  
R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881

R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715  
 R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041  
 R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970  
 R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696  
 R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307  
 R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945  
 R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896  
 R-nnnnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396  
 R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282  
 R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477  
 R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315  
 R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884  
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521  
 R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168  
 R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163  
 R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526  
 R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792  
 R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090  
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126  
 R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127  
 R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491



R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58/  
/Hs.48824:D87717

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75/  
/Hs.153563:AF011333

R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709

R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320

R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cd  
s//1.4e-116:559:97//Hs.28307:AF071185

R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//H  
s.79706:U53204

R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013

R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.  
norvegicus] //4.3e-25:137:98//Hs.5337:AA243757

R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514

R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830

R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827

R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670

R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, com  
plete cds//1.2e-107:541:95//Hs.33787:AF037261

R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71/  
/Hs.95140:D80011

R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820

R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:8  
8//Hs.154326:D42087

R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481

R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165

R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679

R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732

R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892

R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085  
R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124  
:AF019369  
R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405  
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3  
e-30:162:99//Hs.5734:AB014579  
R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs  
.155464:AF088219  
R-nnnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064  
R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptid  
e 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682  
R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:29  
0:85//Hs.113283:AF018080  
R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480  
R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577  
R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827  
R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366  
R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTE  
IN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5  
.6e-34:280:79//Hs.114905:AA088442  
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub  
unit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182  
R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627  
R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF0  
10238  
R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903  
R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:43  
4:99//Hs.14146:W92235  
R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402

R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249

R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219

R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223

R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155

R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624

R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058

R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751

R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845

R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615

R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670

R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933

R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389

R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000

R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804

R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540

R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943

R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265

R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817

R-HEMBA1003222//ESTs, Weakly similar to weak similarity to HSP90 [C.eleg

ans] //1.1e-42:310:85//Hs.23294:W27666  
R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305  
R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834  
R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864  
R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929  
R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219  
R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392  
R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785  
R-HEMBA1003281  
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109  
R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266  
R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353  
R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872  
R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869  
R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119  
R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173  
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029  
R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357  
R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540  
R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651

R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588  
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247  
 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363  
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847  
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127  
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204  
 R-nnnnnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309  
 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563  
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013  
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:5  
 44:98//Hs.25812:AF058696  
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121  
 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516  
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:52  
 9:84//Hs.113283:AF018080  
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688  
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760  
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058  
 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817  
 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673  
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sa  
 piens]//2.8e-93:495:93//Hs.91619:AA552351  
 R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734  
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522  
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058  
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [  
 H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440  
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//

Hs.46918:AF052099  
R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892  
R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065  
R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212  
R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087  
R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042  
R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374  
R-HEMBA1003615  
R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167  
R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387  
R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888  
R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021  
R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438  
R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830  
R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010  
R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783  
R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957  
R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049  
R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635  
R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329  
R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083

R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens] //1.1e-101:528:95//Hs.22934:AA581379

R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916

R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873

R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064

R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777

R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080

R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823

R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847

R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839

R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592

R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans] //4.6e-70:348:96//Hs.11282:AI147040

R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247

R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089

R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus] //1.9e-77:364:100//Hs.12152:AA156214

R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans] //2.1e-101:558:93//Hs.18171:AA524327

R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600

R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236

R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans] //2.8e-16:93:100//Hs.107747:AI357868

R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295

R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344

R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163

R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219

R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C HAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161

R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033

R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547

R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911

R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621

R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930

R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179

R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788

R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187

R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659

R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157

R-HEMBA1003939

R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669

R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545

R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591

R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562

R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253

R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525

R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882

R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT



RY !!!! [H.sapiens] //2.2e-91:448:97//Hs.117834:AA766771  
 R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756  
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:8  
 1//Hs.150275:D87682  
 R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105  
 R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899  
 R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011  
 R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774  
 R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461  
 R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191  
 R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253  
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens] //1.5e-  
 22:365:70//Hs.99692:AA811804  
 R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469  
 R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M117  
 17  
 R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754  
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:57  
 7:82//Hs.113283:AF018080  
 R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988  
 R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652  
 R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251  
 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:6  
 9//Hs.90998:D50918  
 R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562  
 R-HEMBA1004133  
 R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736  
 R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320  
 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs

.155464:AF088219  
R-HEMBA1004150//GRANALCALCIN//0.99:357:59//Hs.79381:M81637  
R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:8  
4//Hs.154326:D42087  
R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96  
//Hs.59988:AF067855  
R-HEMBA1004199  
R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701  
R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea m  
ays] //1.7e-107:552:94//Hs.10092:AI189282  
R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.  
5e-96:275:98//Hs.15832:AB014518  
R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748  
R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617  
R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN  
G ENTRY !!!! [H.sapiens] //4.0e-16:117:91//Hs.92033:AA255832  
R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:  
83//Hs.153014:AB002353  
R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389  
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511  
:72//Hs.154103:AF061258  
R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE  
PROTEIN CL-6 [Rattus norvegicus] //2.1e-61:221:86//Hs.7089:W37284  
R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962  
R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN  
G ENTRY !!!! [H.sapiens] //1.4e-89:465:95//Hs.113660:D20018  
R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931  
R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//  
1.4e-111:553:96//Hs.93677:AF091081

R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rat  
tus norvegicus; Bos taurus] //4.4e-92:559:89//Hs.28298:AA203228

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA  
, complete cds//6.2e-108:538:97//Hs.101766:AF022795

R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferr  
ing//1.7e-34:223:75//Hs.81884:U13061

R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat reg  
ion of Fowlpox virus BamHI-orf7 protein [C.elegans] //3.6e-93:496:94//Hs.  
14337:AA534961

R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426

R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679

R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199  
:X16281

R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904

R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714

R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561

R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231

R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336

R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240

R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cd  
s//1.3e-75:444:90//Hs.80686:D89667

R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:  
83//Hs.153014:AB002353

R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576  
:93//Hs.55458:X77494

R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869

R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057

R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264

R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084

R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219

R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717

R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933

R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518

R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503

R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829

R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033

R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172

R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306

R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034

R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941

R-HEMBA1004507

R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271

R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947

R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972

R-HEMBA1004554

R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913

R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243

R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769

R-nnnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661  
 R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0501//4.6e-52:327:85//Hs.159897:AB007970  
 R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915  
 R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785  
 R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152  
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN RO  
 5D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12  
 263:AA282393  
 R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454  
 R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442  
 R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348  
 R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560  
 R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368  
 R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252  
 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562  
 R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042  
 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881  
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs  
 .155464:AF088219  
 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235  
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467:73//  
 Hs.91916:AF035317  
 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151  
 R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275  
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation  
 groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828  
 R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651

R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428  
R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081  
R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L0649  
8  
R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679  
R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504  
R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380  
R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705  
R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092  
R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633  
R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476  
R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167  
R-aaaaaaaaaaaaaaaa  
R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732  
R-HEMBA1004806  
R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676  
R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784  
R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002  
R-HEMBA1004847  
R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120  
R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267  
R-HEMBA1004864  
R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362  
R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409  
R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676  
R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470  
R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011

R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388

R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053

R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053

R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883

R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215

R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434

R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007

R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074

R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040

R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035

R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065

R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404

R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683

R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329

R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894

R-HEMBA1004995

R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520

R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548

R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM

OLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382  
R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:8  
5//Hs.22271:D26067  
R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens] /  
/2.6e-48:443:78//Hs.139019:N99348  
R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Can  
is familiaris] //1.2e-87:542:87//Hs.16258:AI376436  
R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145  
R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451  
R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.7938  
5:U90905  
R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789  
R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U  
17077  
R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958  
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete  
cds//1.7e-111:545:96//Hs.11170:AF080561  
R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739  
R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952  
R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85/  
/Hs.19949:X98173  
R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0488//4.7e-36:394:75//Hs.67619:AB007957  
R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-3  
2:362:77//Hs.132206:AF039694  
R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397  
R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914  
R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766  
R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239



R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) m  
RNA, complete cds//0.84:191:61//Hs.26931:AF061836

R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284

R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687

R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331

R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834

R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896

R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1  
e-49:277:93//Hs.72660:AB011157

R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862

R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391

R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750

R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs  
.155464:AF088219

R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs  
.32567:AF073519

R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046

R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169

R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472

R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83  
733:X15606

R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467

R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp  
lete cds//4.7e-46:294:81//Hs.129735:AF010144

R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0  
:210:62//Hs.4:X03350

R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653

R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305

R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.544  
86:X54150

R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cdna yk3  
0b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568

R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278

R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725

R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059

R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)  
mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248

R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//  
Hs.136309:AB007960

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87/  
/Hs.6445:L40391

R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961

R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494

R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:  
85//Hs.153014:AB002353

R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
8.4e-73:464:87//Hs.103948:K00627

R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445

R-HEMBA1005497

R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788

R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis,  
mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544

R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870

R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans  
]//2.6e-82:387:99//Hs.67466:AI219740

R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322

R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045  
 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:  
 179:84//Hs.42674:U61981  
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788  
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer  
 evisiae]//8.6e-115:578:95//Hs.17035:AI080471  
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350  
 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926  
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627  
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:  
 439:91//Hs.22897:R43193  
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103  
 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709  
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497  
 R-HEMBA1005577  
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64  
 //Hs.57929:AB011538  
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392  
 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539  
 R-HEMBA1005588//Human: c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990  
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905  
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820  
 R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125  
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390  
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422  
 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisi  
 ae]//2.8e-95:539:92//Hs.19400:AA662845  
 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:3

17:78//Hs.1721:X58377

R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081

R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522

R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.10458:AF088219

R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973

R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477

R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450

R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258

R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:U44060

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406

R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055

R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943

R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP) //1.2e-45:398:79//Hs.155481:AJ006470

R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815

R-nnnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672

R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096

R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:U21936

R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974

R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.10458:AF088219

R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601

R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960  
 R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201  
 R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618  
 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911  
 R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917  
 R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970  
 R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252  
 R-HEMBA1005894  
 R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686  
 R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363  
 R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632  
 R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.  
 5e-45:446:75//Hs.59403:AB011098  
 R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867  
 R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418  
 R-HEMBA1005963  
 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, comple  
 te cds//2.2e-113:580:95//Hs.26285:AF082516  
 R-HEMBA1005991//Human antiseecretory factor-1 mRNA, complete cds//2.0e-45  
 :551:70//Hs.148495:AF050199  
 R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618  
 R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875  
 R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4  
 e-28:444:67//Hs.26450:AB018268  
 R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951  
 R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508  
 R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490  
 R-nnnnnnnnnnnnn

R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612  
R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517  
R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313  
R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA,  
complete cds//3.4e-43:328:82//Hs.73614:U83460  
R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297  
R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293  
R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931  
R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.  
7e-27:296:73//Hs.119387:AB007958  
R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542  
R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212  
R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U3193  
0  
R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627  
R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906  
R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125  
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97/  
/Hs.109268:AF070557  
R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus m  
usculus] //3.3e-114:581:95//Hs.23617:AA928683  
R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:7  
6//Hs.74554:D38522  
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5  
.7e-30:179:91//Hs.15836:AF083384  
R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84/  
/Hs.41742:AB007881  
R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive

[M.musculus] //1.2e-97:529:93//Hs.10552:AA524401  
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE  
[H.sapiens] //2.7e-88:484:92//Hs.104129:AA923278  
R-nnnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770  
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDI  
NG PROTEIN NAB2 [S.cerevisiae] //1.6e-66:377:91//Hs.108674:W25821  
R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735  
R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019  
R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037  
R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:16  
7:86//Hs.74478:U33931  
R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculu  
s] //5.6e-76:417:94//Hs.111754:AI204587  
R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs  
.155464:AF088219  
R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518  
:U49184  
R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//  
Hs.79706:U53204  
R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN  
SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae] //3.6e-119:582:9  
7//Hs.42343:AI417075  
R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382  
R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008  
R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787  
R-HEMBA1006377//EST//0.0097:145:62//Hs.133027:AI049830  
R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0  
e-41:349:79//Hs.154872:AB011166  
R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651

R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0  
e-87:582:84//Hs.23094:M19503

R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923

R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778

R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878

R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13  
:263:66//Hs.43127:AA258004

R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964

R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380

R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:  
487:58//Hs.32963:D31784

R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895

R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-  
17:342:63//Hs.111730:AA604403

R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441

R-HEMBA1006474

R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete  
cds//4.2e-40:365:78//Hs.46468:U45984

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.13  
2243:Y07701

R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223

R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350

R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720

R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387

R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117

R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:  
135:72//Hs.2161:M62505

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9



e-117:570:96//Hs.153858:AB014566  
R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300  
R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628  
R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934  
R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331  
R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2  
e-48:287:91//Hs.79507:AB011154  
R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated  
protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594  
R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064  
R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876  
R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725  
R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876  
R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.  
5e-29:276:76//Hs.144563:AF057280  
R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390  
R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs  
.155464:AF088219  
R-HEMBA1006612  
R-HEMBA1006617//ESTs//1.2e-25:225:80//Hs.138852:AA284247  
R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630  
R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:9  
0//Hs.22271:D26067  
R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNIN  
G ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889  
R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [  
Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185  
R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777  
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete

cds//8.1e-108:567:94//Hs.6196:U40282  
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511  
 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102  
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594  
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842  
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435  
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apar-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263  
 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695  
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens] //1.1e-92:483:94//Hs.6525:AI205313  
 R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062  
 R-HEMBA1006717  
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002  
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627  
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099  
 R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646  
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763  
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881  
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562  
 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936  
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705  
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978  
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333  
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305  
 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272

R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556  
R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:8  
3//Hs.154326:D42087  
R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.  
8e-67:611:74//Hs.15519:AB018315  
R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453  
R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739  
R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117  
R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:21  
3:84//Hs.9096:AA029400  
R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308  
R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712  
R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382  
R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein/  
/6.5e-77:371:98//Hs.42644:AJ010841  
R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321  
R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457  
R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827  
R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:3  
68:80//Hs.149323:AB002325  
R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679  
R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440  
R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293  
R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-1  
12:558:96//Hs.107905:AI248363  
R-HEMBA1007045  
R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788  
R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839

R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140  
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272  
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866  
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING  
 ENTRY !!!! [H.sapiens]//7.2e-40:163:83//Hs.152369:AA504818  
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087  
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025  
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597  
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121  
 493:D25272  
 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438  
 R-HEMBA1007147  
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818  
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674  
 R-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:9  
 4//Hs.22396:AF062085  
 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954  
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.  
 7e-62:332:95//Hs.3363:D86987  
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990  
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4  
 e-98:471:97//Hs.27197:AB018340  
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864  
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934  
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83/  
 /Hs.43681:AL022394  
 R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062  
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207

R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543  
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804  
 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990  
 R-HEMBA1007301  
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917  
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens] //5.5e-15:311:64//Hs.142764:AA205569  
 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629  
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452  
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848  
 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684  
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333  
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens] //3.3e-44:341:71//Hs.111730:AA604403  
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member L1 GHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090  
 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969  
 R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418  
 R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332  
 R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449  
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C3 4E10.1 IN CHROMOSOME III [Caenorhabditis elegans] //6.0e-92:477:95//Hs.4877:AA418465  
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928

R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702  
 R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954  
 R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:AI357802  
 R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903  
 R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107  
 R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUC  
 TASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//H  
 s.116490:AA659584  
 R-HEMBB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939  
 R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:  
 80//Hs.4953:D63997  
 R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:  
 70//Hs.153014:AB002353  
 R-HEMBB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193  
 R-HEMBB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5  
 e-18:298:69//Hs.153026:AB014540  
 R-HEMBB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239  
 R-HEMBB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521  
 R-HEMBB1000136//ESTs//0.043:262:59//Hs.61304:AA025692  
 R-HEMBB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915  
 R-HEMBB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951  
 R-HEMBB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223  
 R-HEMBB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558  
 R-HEMBB1000198//ESTs//1.0:123:62//Hs.116602:AA665965  
 R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:  
 86//Hs.153014:AB002353  
 R-HEMBB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364  
 R-HEMBB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF  
 F40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019

R-HEMBB1000226//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B04  
95.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214  
R-HEMBB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106  
R-HEMBB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs  
.155464:AF088219  
R-HEMBB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783  
R-HEMBB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782  
R-HEMBB1000264  
R-HEMBB1000266//ESTs, Weakly similar to similar to the beta transducin f  
amily [C.elegans]//2.7e-102:556:93//Hs.16079:AA083522  
R-HEMBB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385  
R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9  
e-24:198:72//Hs.101414:AB011129  
R-HEMBB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458  
R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:  
87//Hs.153014:AB002353  
R-HEMBB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601  
R-HEMBB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034  
R-HEMBB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs  
.155464:AF088219  
R-HEMBB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576  
R-HEMBB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480  
R-HEMBB1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084  
R-HEMBB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs  
.155464:AF088219  
R-HEMBB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736  
R-HEMBB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651  
R-HEMBB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020  
R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:

65//Hs.36232:D80008

R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590

R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487//2.3e-56:335:77//Hs.92381:AB007956

R-HEM BB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.  
66710:X96969

R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840

R-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8  
e-109:531:97//Hs.16184:AJ001642

R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72/  
/Hs.19949:X98173

R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026

R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591

R-HEM BB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:8  
9//Hs.154326:D42087

R-HEM BB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !  
!!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303

R-HEM BB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990

R-HEM BB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221

R-HEM BB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438

R-HEM BB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396

R-HEM BB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:9  
0//Hs.40100:AB002390

R-HEM BB1000487//EST//0.78:87:68//Hs.134601:AI081506

R-HEM BB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs  
.155464:AF088219

R-HEM BB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:31  
2:76//Hs.113283:AF018080

R-HEM BB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125



R-HEM BB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703

R-HEM BB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087

R-HEM BB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080

R-HEM BB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099

R-HEM BB1000550//EST//2.9e-11:113:79//Hs.161503:N68662

R-HEM BB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288

R-HEM BB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986

R-HEM BB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258

R-HEM BB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709

R-HEM BB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618

R-HEM BB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247

R-HEM BB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895

R-HEM BB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704

R-HEM BB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391

R-HEM BB1000598//Human antisecretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199

R-HEM BB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125

R-HEM BB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

R-HEM BB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152

R-HEM BB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531

R-HEM BB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522

R-HEM BB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582

R-HEM BB1000643//ESTs//0.0049:191:62//Hs.55445:W31963

R-HEM BB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100

R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939.  
 R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988  
 R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705  
 R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293  
 R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454  
 R-nnnnnnnnnnnnn//Homo sapiens neuroanl mRNA, complete cds//6.5e-52:287:93  
 //Hs.158300:AF040723  
 R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs  
 .155464:AF088219  
 R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412  
 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-  
 50:245:99//Hs.111730:AA604403  
 R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//  
 Hs.10351:AB002306  
 R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881  
 R-HEMBB1000738//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121  
 493:D25272  
 R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925  
 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522  
 R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445  
 R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541  
 R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771  
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73  
 734:Z23091  
 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718  
 R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961  
 R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs  
 .155464:AF088219  
 R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447

R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124  
 R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs  
 .155464:AF088219  
 R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881  
 R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176  
 R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545  
 R-HEMBB1000840//ATPase, Na+/K+ transporting, beta 2 polypeptide//1.3e-43  
 :163:84//Hs.78854:AF007876  
 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.  
 5e-41:367:78//Hs.129740:AB011137  
 R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599  
 R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1  
 .0e-41:483:73//Hs.2379:U23942  
 R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141  
 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247  
 R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740  
 R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258  
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.  
 51048:X68830  
 R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881  
 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066  
 R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983  
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:3  
 67:73//Hs.149323:AB002325  
 R-HEMBB1000915//ESTs//0.00018:188:61//Hs.144847:AI222742  
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84/  
 /Hs.127649:AB007874  
 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784  
 R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:35

0:91//Hs.49163:AA532881  
 R-HEM BB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1  
 e-84:546:86//Hs.23094:M19503  
 R-HEM BB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354  
 R-HEM BB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007  
 R-HEM BB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242  
 R-HEM BB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369  
 R-HEM BB1000991//EST//0.99:58:72//Hs.100246:T23625  
 R-HEM BB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482  
 :70//Hs.154103:AF061258  
 R-HEM BB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112  
 R-HEM BB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapie  
 ns] //2.3e-25:339:71//Hs.129992:H58762  
 R-HEM BB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214  
 R-HEM BB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814  
 R-HEM BB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:30  
 5:76//Hs.113283:AF018080  
 R-HEM BB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562  
 R-HEM BB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385  
 R-HEM BB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975  
 R-HEM BB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107  
 R-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.  
 1e-87:497:91//Hs.15832:AB014518  
 R-HEM BB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.  
 2e-26:125:81//Hs.5737:AB007944  
 R-HEM BB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785  
 R-HEM BB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381  
 R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:51  
 2:97//Hs.12953:AF034803

R-HEM BB1001096//Human HsLIM15 mRNA for HsLim15, complete cds//1.2e-20:23  
3:70//Hs.37181:D64108

R-HEM BB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:  
82//Hs.153014:AB002353

R-HEM BB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:29  
6:87//Hs.113283:AF018080

R-HEM BB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426

R-HEM BB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092

R-HEM BB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942

R-HEM BB1001126

R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subuni  
t mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077

R-HEM BB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962

R-HEM BB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881

R-HEM BB1001151

R-HEM BB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197

R-HEM BB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878

R-nnnnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162

R-HEM BB1001177

R-HEM BB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349

R-HEM BB1001199

R-HEM BB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183

R-HEM BB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549

R-HEM BB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573

R-HEM BB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8  
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti  
body IA4))//3.1e-44:298:87//Hs.103458:X53795

R-HEM BB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817

R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus] //3.8e-80:400:96//Hs.71873:AA148213

R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560

R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236

R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987

R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268

R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970

R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087

R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412

R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans] //2.6e-104:515:97//Hs.16606:W81021

R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840

R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112

R-HEMBB1001302

R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627

R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627

R-HEMBB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873

R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754

R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens] //6.5e-61:313:96//Hs.43071:AA206222

R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365

R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639

R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470

R-HEMBB1001346

R-HEM BB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354  
 R-HEM BB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721  
 R-HEM BB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055  
 R-HEM BB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:7  
 2//Hs.154326:D42087  
 R-HEM BB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617  
 R-HEM BB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs  
 .155464:AF088219  
 R-HEM BB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205  
 R-HEM BB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699  
 R-HEM BB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970  
 R-HEM BB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350  
 R-HEM BB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:3  
 65:58//Hs.389:X76342  
 R-HEM BB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644  
 R-HEM BB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651  
 R-HEM BB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846  
 R-HEM BB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317  
 R-HEM BB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201  
 R-HEM BB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236  
 R-HEM BB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515  
 R-HEM BB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293  
 R-HEM BB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78/  
 /Hs.41742:AB007881  
 R-HEM BB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:6  
 1//Hs.13275:AI341468  
 R-HEM BB1001482//ESTs, Moderately similar to zinc finger protein [R.norve  
 gicus]//0.80:53:83//Hs.26799:W74481

R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515  
R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280  
R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915  
R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159  
R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459  
R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353  
R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869  
R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274  
R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962  
R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA535216  
R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329  
R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944  
R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219  
R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015  
R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184  
R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044  
R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888  
R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272  
R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082  
R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633  
R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813



R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438  
 R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577  
 R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572  
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.  
 9e-117:573:97//Hs.24439:AB014546  
 R-HEMBB1001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:  
 523:97//Hs.26939:AA804534  
 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358  
 R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867  
 R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038  
 R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080  
 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sa  
 piens]//4.9e-32:277:73//Hs.142764:AA205569  
 R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645  
 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO  
 MOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113  
 R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403  
 R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488  
 R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287  
 R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059  
 R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211  
 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:  
 74//Hs.70008:L00352  
 R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369  
 R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406  
 R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253  
 R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391  
 R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247

R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503

R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI P1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209

R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0488//9.6e-39:288:73//Hs.67619:AB007957

R-HEMBB1001839

R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125

R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539

R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106

R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397

R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434

R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA487980

R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572

R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240

R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081

R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310

R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191

R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725

R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915

R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216

R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750

R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897

R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390

R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:70//Hs.153086:Y11251

R-HEM BB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:1  
99:77//Hs.149323;AB002325

R-HEM BB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875

R-HEM BB1001944//EST//0.034:228:57//Hs.93664:N23366

R-HEM BB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875

R-HEM BB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589

R-HEM BB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998

R-HEM BB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:8  
3//Hs.74554:D38522

R-HEM BB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881

R-HEM BB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972

R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.  
3e-61:296:88//Hs.153468:AB011147

R-HEM BB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531

R-HEM BB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475

R-HEM BB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572

R-HEM BB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223

R-HEM BB1001996

R-HEM BB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798

R-HEM BB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
3.0e-18:222:71//Hs.103948:K00627

R-HEM BB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334

R-HEM BB1002009//EST//2.9e-44:245:94//Hs.28788:R66896

R-HEM BB1002015//EST//0.0027:198:63//Hs.160868:AI359052

R-HEM BB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900

R-HEM BB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426

R-HEM BB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638

R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:30

1:85//Hs.113283:AF018080

R-HEM BB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638

R-HEM BB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840

R-HEM BB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671

R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144

R-HEM BB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193

R-HEM BB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881

R-HEM BB1002115

R-HEM BB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814

R-HEM BB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006

R-HEM BB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553

R-HEM BB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073

R-HEM BB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185

R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934

R-HEM BB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881

R-HEM BB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841

R-HEM BB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584

R-HEM BB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631

R-HEM BB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807

R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503

R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363

R-HEM BB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112

R-HEM BB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223

R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305  
 R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67/  
 /Hs.155174:AB007892  
 R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637  
 R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312  
 R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228  
 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein/  
 /0.85:46:84//Hs.42644:AJ010841  
 R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322  
 R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613  
 R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:6  
 5//Hs.74554:D38522  
 R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085  
 R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs  
 .142296:AF072467  
 R-HEMBB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055  
 R-HEMBB1002387  
 R-HEMBB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//2.3e-23:168:77//Hs.133526:N21103  
 R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.  
 2e-57:304:90//Hs.144563:AF057280  
 R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293  
 R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:  
 87//Hs.153014:AB002353  
 R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:7  
 1//Hs.154326:D42087  
 R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089  
 R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083  
 R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176

R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969  
R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017  
R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98/  
/Hs.141515:T41142  
R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615  
R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.  
2e-48:265:95//Hs.48827:AA873278  
R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538  
R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, comp  
lete cds//0.50:142:69//Hs.159301:U43672  
R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605  
R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478  
R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259  
R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C  
.elegans]//5.1e-22:210:81//Hs.11896:T68813  
R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.  
51048:X68830  
R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189  
R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045  
R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138  
R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:8  
7//Hs.154326:D42087  
R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424  
R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923  
R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881  
R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896  
R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265  
R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0508//8.5e-47:278:83//Hs.159187:AB007977  
R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150  
R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917  
R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247  
R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219  
R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881  
R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:AI419775  
R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase //8.6e-54:543:75//Hs.2638:Z28339  
R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646  
R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753  
R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099  
R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487  
R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398  
R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842  
R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547  
R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682  
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701  
R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219  
R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152  
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901  
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304  
R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165

R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350

R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531

R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065

R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099

R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241

R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713

R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352

R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172

R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577

R-MAMMA1000133

R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017

R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970

R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881

R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263

R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787

R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162

R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069

R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611



R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054  
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881  
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.muscu  
lus] //1.4e-41:272:90//Hs.68398:AA421103  
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425  
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946  
R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.  
3e-47:322:86//Hs.15519:AB018315  
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LI  
GHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090  
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041  
R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF0  
10238  
R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814  
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0508//2.7e-57:304:78//Hs.159187:AB007977  
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124  
:AF019369  
R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694  
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487//3.1e-58:295:83//Hs.92381:AB007956  
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066  
R-MAMMA1000287  
R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.  
155174:AB007892  
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:7  
6//Hs.22271:D26067  
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251  
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434

R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491

R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]  
//8.6e-54:278:97//Hs.139170:AA662998

R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881

R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.8  
2:204:61//Hs.154919:AB014525

R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159

R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces  
cerevisiae] //0.42:172:61//Hs.11463:AA535912

R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:8  
2//Hs.154326:D42087

R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659

R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523

R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065

R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto  
r, complete cds//8.6e-14:106:92//Hs.32170:AB015132

R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AI301060

R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLY  
PROTEIN [Mus musculus] //9.1e-47:316:81//Hs.138698:N38973

R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198

R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.  
3e-27:304:72//Hs.119387:AB007958

R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099

R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA,  
complete cds//1.5e-58:282:82//Hs.97203:U83171

R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081

R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067

R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:8  
1//Hs.40100:AB002390

R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452

R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461

R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171

R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179

R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447

R-MAMMA1000458

R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176

R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361

R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959

R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886

R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759

R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219

R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390

R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390

R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267

R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236

R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131

R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561

R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211

R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872

R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548

R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219

R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042

R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267

R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105

R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180

R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361

R-MAMMA1000623

R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002

R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203

R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162

R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3' REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065

R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476

R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212

R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343

R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644

R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333

R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569

R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515

R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329

R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942

R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267  
 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893  
 R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1  
 098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141  
 429:AA631915  
 R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:2  
 53:98//Hs.31575:AF100141  
 R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis a  
 ntheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632  
 288  
 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205  
 R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3  
 e-90:568:86//Hs.23094:M19503  
 R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627  
 R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131  
 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256  
 R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:  
 76//Hs.153014:AB002353  
 R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204  
 R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439  
 R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150  
 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163  
 R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73  
 919:X81637  
 R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA572675  
 R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881  
 R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902  
 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358

R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097  
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955  
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251  
R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390  
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212  
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311  
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922  
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099  
R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399  
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875  
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243  
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128  
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166  
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107  
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215  
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329  
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093  
R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634  
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989  
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696  
R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335  
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727  
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281

R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428  
R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducibl  
e), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053  
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178  
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8  
2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti  
body IA4))//7.5e-49:340:85//Hs.103458:X53795  
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.  
0e-48:216:85//Hs.153468:AB011147  
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881  
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204  
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0  
e-39:338:79//Hs.93121:AB018304  
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881  
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apa  
f-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263  
R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82/  
/Hs.80738:X52075  
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:9  
7//Hs.25863:AA630313  
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86/  
/Hs.153563:AF011333  
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814  
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536  
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461  
R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:9  
1//Hs.40100:AB002390  
R-nnnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650  
R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881

R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1  
 .7e-13:273:65//Hs.98738:AI015487

R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532

R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748

R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:  
 68//Hs.153014:AB002353

R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944

R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7  
 e-84:556:85//Hs.23094:M19503

R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222

R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926

R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2  
 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587

R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete c  
 ds//4.2e-27:232:76//Hs.61840:U28686

R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576

R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,  
 3429 nt]//8.8e-53:462:78//Hs.116007:S79267

R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-5  
 9:460:81//Hs.5247:AF029750

R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029

R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399

R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF06  
 8179

R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131

R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-5  
 8:409:84//Hs.5247:AF029750

R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:  
 99//Hs.129982:AI420970



R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251  
R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959  
R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519  
R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202  
R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348  
R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637  
R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148  
R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293  
R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202  
R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315  
R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701  
R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619  
R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307  
R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569  
R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149  
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561  
R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001  
R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643  
R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144  
R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371  
R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876  
R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.

2e-27:348:70//Hs.15731:AB011135  
R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426  
R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete  
cds//4.0e-43:300:85//Hs.46468:U45984  
R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, com  
plete cds//8.8e-12:188:70//Hs.55771:AF004709  
R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471  
R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426  
R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs  
.32567:AF073519  
R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127  
R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478  
R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322  
R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216  
R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881  
R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831  
R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275  
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, comp  
lete cds//1.6e-19:117:96//Hs.19122:AF038957  
R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267  
R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168  
R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618  
R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67  
//Hs.155174:AB007892  
R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542  
R-MAMMA1001465  
R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) m  
RNA, complete cds//0.79:182:66//Hs.136529:AF058317  
R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78/

/Hs.43681:AL022394

R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065

R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522

R-MAMMA1001510

R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242

R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969

R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696

R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140

R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305

R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441

R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

R-MAMMA1001604

R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616

R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272

R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315

R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074

R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377

R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp

lete cds//1.7e-54:272:81//Hs.129735:AF010144  
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs  
.155464:AF088219  
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248  
R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.0  
66:196:62//Hs.159161:X69550  
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081  
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0488//1.0e-17:246:73//Hs.67619:AB007957  
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:  
89//Hs.3094:D31884  
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088  
R-MAMMA1001715//ESTs//1.2e-73:399:93//Hs.124620:AI082338  
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596  
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus ga  
llus] //3.7e-110:552:96//Hs.6923:AI161158  
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651  
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666  
R-MAMMA1001744  
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817  
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041  
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413  
R-MAMMA1001757//ESTs//1.0e-98:488:96//Hs.45184:C14904  
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276  
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847  
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:2  
99:85//Hs.149323:AB002325  
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825  
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.musculus]//7

.6e-43:257:91//Hs.7634:AA481246  
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA,  
complete cds//5.6e-42:272:86//Hs.73614:U83460  
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238  
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644  
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744  
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313  
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892  
R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659  
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:  
87//Hs.44106:D86979  
R-MAMMA1001818  
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881  
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs  
.32567:AF073519  
R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140  
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83/  
/Hs.43681:AL022394  
R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811  
R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461  
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs  
.155464:AF088219  
R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840  
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.  
8e-31:262:77//Hs.5737:AB007944  
R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-0  
6:450:58//Hs.132206:AF039694  
R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA,  
complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1  
 .2e-46:429:78//Hs.2379:U23942

R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD8  
 2 antigen (R2 leukocyte antigen, antigen detected by monoclonal and anti  
 body IA4))//6.7e-47:283:89//Hs.103458:X53795

R-nnnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.  
 4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]  
 //6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs  
 .155464:AF088219

R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mR  
 NA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs  
 .32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete  
 cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:78//Hs.138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487//6.2e-51:318:82//Hs.92381:AB007956

R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2  
e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phos  
phate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U486  
96

R-MAMMA1002236

R-MAMMA1002243

R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:29  
9:87//Hs.113283:AF018080

R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772

R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141

R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751

R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//  
1.7e-39:203:81//Hs.154257:AI275982

R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881

R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454

R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153

R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO  
MOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359

R-MAMMA1002308

R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mR  
NA//2.2e-44:280:87//Hs.154069:U06452



R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3  
e-70:503:81//Hs.23094:M19503

R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094

R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.  
3e-49:457:76//Hs.144563:AF057280

R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183

R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084

R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658

R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//  
Hs.91916:AF035317

R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897

R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618

R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439

R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127

R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-5  
8:259:92//Hs.43628:Y15228

R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:7  
7//Hs.40100:AB002390

R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367

R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73  
919:X81637

R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:48  
3:84//Hs.113283:AF018080

R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475

R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2  
(XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587

R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236

R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542

R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs

.155464:AF088219

R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061

R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845

R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294

R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488

R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588

R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477

R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475

R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348

R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996

R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.89121:AB007954

R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076

R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106

R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496

R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103

R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460

R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293

R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664

R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214

R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147

R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851

R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058

R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681

R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693

R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433

R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371

R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258

R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:M29874

R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737

R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369

R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053

R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389

R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670

R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306

R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081

R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881

R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R. norvegicus]//2.3e-35:308:79//Hs.93332:AA811920

R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complet

e cds//9.7e-57:283:86//Hs.115325:D84488  
R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:8  
9//Hs.40100:AB002390  
R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421  
R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915  
R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776  
R-MAMMA1002655  
R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75  
//Hs.97476:AB007886  
R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:8  
2//Hs.154326:D42087  
R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk5  
2e10.5 [C.elegans]//5.3e-108:544:96//Hs.16464:W19606  
R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213  
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.  
6e-109:544:96//Hs.3363:D86987  
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385  
R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675  
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510  
R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//6.9e-70:353:96//Hs.138404:R70986  
R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234  
R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858  
R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89/  
/Hs.153563:AF011333  
R-MAMMA1002727//ESTs//2.9e-84:395:100//Hs.162826:AA679571  
R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs  
.155464:AF088219  
R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757

R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907  
R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452  
R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776  
R-MAMMA1002758  
R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281  
R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651  
R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272  
R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750  
R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145  
R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812  
R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198  
R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260  
R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319  
R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881  
R-MAMMA1002835  
R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723  
R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395  
R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238  
R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081  
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067  
R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941  
R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592  
R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194  
R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871  
R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs

.155464:AF088219

R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811

R-MAMMA1002890//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEE  
SB82F [*C.elegans*]//4.2e-92:438:99//Hs.155871:AA533783

R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:32  
2:80//Hs.26929:AF008915

R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087

R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF06  
8179

R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:7  
6//Hs.90981:D80002

R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881

R-MAMMA1002938

R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1  
e-83:556:85//Hs.23094:M19503

R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243

R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:  
77//Hs.153014:AB002353

R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081

R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [*H.sapiens*]//9.6e-104:5  
25:95//Hs.94396:AA399630

R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835

R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279

R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF  
F40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019

R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF06  
8179

R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857

R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617

R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus] //1.4e-53:320:90//Hs.92023:AI022248  
 R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189  
 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268  
 R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315  
 R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //3.5e-27:257:77//Hs.96337:AA225358  
 R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321  
 R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160  
 R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940  
 R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941  
 R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862  
 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348  
 R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881  
 R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559  
 R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus] //1.1e-102:545:93//Hs.13755:AA878911  
 R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969  
 R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] //1.4e-34:421:70//Hs.161959:AA493652  
 R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651  
 R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283  
 R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366  
 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788  
 R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125  
 R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537  
 R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861

R-nnnnnnnnnnnnnnn

R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster] //2.0e-87:524:89//Hs.6884:W30736

R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94/  
/Hs.108112:AF070640

R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312

R-NT2RM4000027

R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663

R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI186169

R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379

R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e  
-113:549:97//Hs.95665:AF070639

R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817

R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708

R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312

R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CY  
TOPLASMIC [H.sapiens] //1.9e-99:536:92//Hs.127810:AI246301

R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397

R-nnnnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962

R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160

R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens] //4.1e-99  
:542:93//Hs.6366:AA614113

R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723

R-NT2RM4000199//ESTs//0.020:95:65//Hs.146203:AI254528

R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876

R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs  
.155464:AF088219

R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.  
7e-103:546:94//Hs.111138:AB018255



R-NT2RM4000215

R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760

R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602

R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031

R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974

R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128

R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673

R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219

R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637

R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579:96//Hs.5216:AA534881

R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479

R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063

R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542

R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140

R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879

R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977

R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285

R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.eleg

ans] //5.4e-75:470:90//Hs.69235:AA192359

R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173

R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687

R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865

R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae] //6.0e-99:492:96//Hs.21090:AA418587

R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens] //2.2e-102:493:97//Hs.111279:W84558

R-NT2RM4000496

R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465

R-NT2RM4000514//ESTs//1.7e-112:552:96//Hs.6686:AA205496

R-nnnnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae] //1.4e-60:343:93//Hs.16014:AA074879

R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731

R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461

R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777

R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198

R-NT2RM4000585//EST//0.28:63:77//Hs.150024:AI291981

R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437

R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891

R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589

R-nnnnnnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697

R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli] //1.4e-102:519:96//Hs.14779:N64822

R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144

R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans] //2.9e-115:55

0:98//Hs.11820:AA205531  
 R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510  
 R-nnnnnnnnnnnnnnn  
 R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128  
 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR  
 ECURSOR [Mus musculus]//2.2e-103:519:95//Hs.6823:W18181  
 R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311  
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6  
 e-105:536:95//Hs.137168:AB018303  
 R-NT2RM4000741//ESTs//0.99:266:58//Hs.142718:AA034046  
 R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988  
 R-NT2RM4000764  
 R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174  
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.  
 3e-106:546:94//Hs.18586:AB007920  
 R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mR  
 NA//6.5e-40:424:73//Hs.154069:U06452  
 R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:AI417008  
 R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//  
 Hs.20991:D31891  
 R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520  
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3'  
 end//2.5e-28:158:96//Hs.118249:M21868  
 R-NT2RM4000813  
 R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]  
 //1.3e-109:539:97//Hs.99636:AI219667  
 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-11  
 2:448:99//Hs.20223:AA482031  
 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864

R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597  
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343  
R-aaaaaaaaaaaaa  
R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN  
G ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514  
R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262  
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887  
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647  
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien  
s]//1.7e-82:414:96//Hs.115342:AA650126  
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8  
e-114:545:97//Hs.19542:AB018272  
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5  
e-114:556:97//Hs.15711:AB014539  
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352  
R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto  
r, complete cds//0.42:133:67//Hs.32170:AB015132  
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300  
R-aaaaaaaaaaaaa//ESTs//3.4e-91:439:99//Hs.103177:W72798  
R-NT2RM4001092//ESTs//1.4e-86:517:89//Hs.132969:Z78324  
R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962  
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276  
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311  
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848  
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085  
R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
G ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174  
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3  
.1e-32:274:70//Hs.2379:U23942

R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849  
 R-NT2RM4001203  
 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307  
 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410  
 R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677  
 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184  
 R-NT2RM4001309  
 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857  
 R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899  
 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352  
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae] //1.9e-105:522:97//Hs.18442:AI129307  
 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339  
 R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476  
 R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211  
 R-NT2RM4001382  
 R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507  
 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790  
 R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus] //4.0e-102:539:94//Hs.15744:AI055859  
 R-NT2RM4001412  
 R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895  
 R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054  
 R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae] //7.4e-108:544:94//Hs.7558:AA526812  
 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277  
 R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739  
 R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067

R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.

0e-104:547:93//Hs.153121:AB014585

R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664

R-NT2RM4001522//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.  
.155464:AF088219

R-NT2RM4001557//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:16  
5:83//Hs.29134:H43072

R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027

R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-  
11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a  
alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6  
-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C  
ontains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z  
98046

R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009

R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946

R-nnnnnnnnnnnnnnn

R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171

R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.

1e-112:565:95//Hs.23255:AB018334

R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079

R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957

R-NT2RM4001650

R-NT2RM4001662

R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.

6e-36:230:70//Hs.7764:AB007938

R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496

R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440

R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686  
R-nnnnnnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465  
R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans] //3.1e-108:563:94//Hs.18510:AA522887  
R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt] //0.083:124:68//Hs.120980:S83390  
R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200  
R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629  
R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740  
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270  
R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956  
R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567  
R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920  
R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839  
R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551  
R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070  
R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619  
R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] //4.1e-10:274:62//Hs.161959:AA493652  
R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans] //3.0e-43:292:86//Hs.14202:N46000  
R-nnnnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280  
R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711  
R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252  
R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149  
R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178

R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438  
R-NT2RM4001930//ESTs//4.1e-84:425:96//Hs.80042:N63143  
R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893  
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-1  
10:556:95//Hs.118631:AF098162  
R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268  
R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]  
//5.7e-62:326:95//Hs.3385:N25917  
R-nnnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9  
e-21:121:98//Hs.8772:AA521097  
R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265  
R-NT2RM4001984  
R-NT2RM4001987  
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528  
R-NT2RM4002018  
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:8  
7//Hs.154326:D42087  
R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435  
R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226  
R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887  
R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF06  
8179  
R-nnnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//  
5.5e-42:554:68//Hs.85313:AF071309  
R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//  
2.3e-43:468:73//Hs.139107:K00629  
R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthet  
ase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416



R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655  
 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528  
 R-NNNNNNNNNNNN//ESTs//1.0:95:69//Hs.25897:W65409  
 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:  
 Y13620  
 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712  
 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987  
 R-NT2RM4002146//ESTs//1.9e-93:439:99//Hs.119295:AA442090  
 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111  
 :560:96//Hs.22464:AF084535  
 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552  
 :72//Hs.154103:AF061258  
 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400  
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343  
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678  
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079  
 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUN  
 D [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984  
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-gl  
 ycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-1  
 00:544:93//Hs.27567:W72190  
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs  
 .155464:AF088219  
 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864  
 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263  
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638  
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461  
 R-NT2RM4002294  
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164

R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498  
R-nnnnnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913  
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198  
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549  
R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594  
R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884  
R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328  
R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:98//Hs.16464:W19606  
R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677  
R-NT2RM4002446  
R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142  
R-NT2RM4002457  
R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890  
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.8765:AF083255  
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:AB014591  
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884  
R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029  
R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464  
R-nnnnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//Hs.31030:H50467  
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788  
R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057  
R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312  
R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINE

NYLTRANSFERASE [Bos taurus] //2.3e-89:435:97//Hs.15830:AA165698  
 R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569  
 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermu  
 s aquaticus thermophilus] //9.6e-28:194:87//Hs.59346:AI126802  
 R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096  
 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081  
 R-NT2RP2000008//Zinc finger protein 37a (K0X 21)//5.2e-25:366:67//Hs.544  
 88:X69115  
 R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713  
 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7  
 e-42:223:96//Hs.8309:AB018290  
 R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol  
 og (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749  
 R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798  
 R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910  
 R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanog  
 aster] //2.3e-35:199:94//Hs.41793:AA775879  
 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus] /  
 /1.4e-78:383:98//Hs.58254:W72881  
 R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097  
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, com  
 plete cds//1.1e-78:379:97//Hs.54877:AF050078  
 R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcr  
 ipt, partial//2.9e-21:232:75//Hs.102576:AJ010230  
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8  
 e-75:378:96//Hs.22926:AB018338  
 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236  
 :63//Hs.41:D90064  
 R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757



R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635

R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865

R-NT2RP2000289

R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249

R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712

R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381

R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398

R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441

R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981

R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103

R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010

R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265

R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425

R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045

R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013  
 R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078  
 R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215  
 R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.  
 .110:AB007896  
 R-nnnnnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348  
 R-NT2RP2000523  
 R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5  
 e-30:167:97//Hs.14409:AB011144  
 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446  
 R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1  
 e-66:335:96//Hs.7314:AB014514  
 R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222  
 R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275  
 R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396  
 R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767  
 R-NT2RP2000678//ESTs//2.6e-53:271:96//Hs.23790:N99347  
 R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368  
 R-NT2RP2000715//EST//1.2e-87:418:99//Hs.139425:AA429279  
 R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965  
 R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642  
 R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419  
 R-NT2RP2000809  
 R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745  
 R-nnnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404  
 R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918  
 R-NT2RP2000819  
 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511  
 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR/

/4.6e-10:247:66//Hs.29352:M31165  
R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:A1206552  
R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345  
R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:AB018284  
R-NT2RP2000892//ESTs//2.8e-50:258:96//Hs.119238:AA476267  
R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266  
R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477  
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:AB018298  
R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021  
R-NT2RP2000970//EST//8.7e-06:255:62//Hs.149202:A1246481  
R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537  
R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521  
R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643  
R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660  
R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108  
R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665  
R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068  
R-NT2RP2001119  
R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348  
R-NT2RP2001137  
R-NT2RP2001149//ESTs//5.1e-66:324:97//Hs.27475:AA704512  
R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:A1188145

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:AB007949

R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287

R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510

R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402

R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358

R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//Hs.44014:AA632298

R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353

R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229

R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775

R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665

R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205

R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//2.3e-43:238:93//Hs.106632:N25679

R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138

R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178

R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028

R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038

R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]//3.9e-74:411:93//Hs.47305:AA195153

R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875

R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:469:97//Hs.20483:AA522505

R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030

R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

R-NT2RP2001427//EST//1.7e-11:107:84//Hs.148584:AI201728



R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:55  
8:97//Hs.7627:AI341556

R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394

R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453

R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765

R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539

R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs  
.155464:AF088219

R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513

R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146

R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL  
AR1//6.7e-106:545:95//Hs.4277:Y14494

R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240

R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3  
(XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586

R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816

R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0488//2.0e-76:387:96//Hs.67619:AB007957

R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60/  
/Hs.119:D14661

R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884

R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995

R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767

R-NT2RP2001613

R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294

R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090

R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845

R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336

R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323

R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579  
 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538  
 R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100  
 R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840  
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EX01a) mRNA, complete cds//  
 2.1e-105:519:96//Hs.47504:AF091754  
 R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037  
 R-NT2RP2001861  
 R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941  
 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088  
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.eleg  
 ans]//6.9e-110:556:95//Hs.23159:AA113849  
 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724  
 R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423  
 R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268  
 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087  
 R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180  
 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594  
 R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588  
 R-NT2RP2001969  
 R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745  
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1  
 [M.musculus]//8.3e-15:118:89//Hs.18760:AA166678  
 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233  
 R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332  
 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627  
 R-NT2RP2002041  
 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938  
 R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895

R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068  
R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091  
R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265  
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//  
Hs.11039:AF052183  
R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524  
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e  
-60:376:89//Hs.155218:AJ007509  
R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000  
R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134  
R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527  
R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268  
R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495  
R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:26  
9:98//Hs.107201:W52859  
R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs.87578:AI125363  
R-NT2RP2002193//ESTs//3.5e-79:453:90//Hs.76578:AI290672  
R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946  
R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499  
R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341  
R-ntnnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus  
]//5.4e-48:238:99//Hs.22583:AA188168  
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cd  
s//1.6e-15:131:83//Hs.150595:AF005418  
R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//  
Hs.92137:M19720  
R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-1  
00:550:91//Hs.4029:Z78373

R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:48  
2:93//Hs.5570:AI377863

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,  
partial cds//4.1e-103:527:94//Hs.24812:AF069532

R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA  
, complete cds//1.2e-112:567:95//Hs.31034:AB015594

R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant m  
RNA, complete cds//1.2e-103:600:89//Hs.109051:AF038958

R-NT2RP2002394//ESTs//0.11:158:65//Hs.28792:AI343467

R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815

R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.  
7e-33:285:80//Hs.15731:AB011135

R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA464020

R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521

R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230

R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233

R-nnnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complet  
e cds//9.9e-115:605:92//Hs.125856:AB005289

R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180

R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.  
5e-107:583:91//Hs.23255:AB018334

R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305

R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-10  
9:570:93//Hs.49476:AF009314

R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325

R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens] //7.5e-118:564:97//Hs.94549:AA149547

R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783

R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170

R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220

R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615

R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881

R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

R-NT2RP2002672

R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB //0.99:184:63//Hs.50727:U43572

R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223

R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210

R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626

R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300

R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.6 6:360:59//Hs.119139:AB011108

R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352

R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131

R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042

R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124

R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94// Hs.17481:AF070537

R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124

R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //1.6e-100:501:97//Hs.136202:AA206578

R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031

R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870

R-NT2RP2002880  
 R-NT2RP2002891  
 R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894  
 R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143  
 R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096  
 R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771  
 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480  
 R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060  
 R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213  
 R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [*Drosophila melanogaster*] //3.1e-119:578:97//Hs.106290:AI125291  
 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329  
 R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [*H.sapiens*] //2.4e-98:467:98//Hs.86337:AA149311  
 R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642  
 R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594  
 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082  
 R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081  
 R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512  
 R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345  
 R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355  
 R-NT2RP2003125  
 R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986  
 R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506  
 R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379  
 R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067

R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952  
R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156  
R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816  
R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074  
R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253  
R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661  
R-NT2RP2003243//ESTs//3.6e-53:300:92//Hs.118793:AA192438  
R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937  
R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859  
R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525  
R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427  
R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106  
R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087  
R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321  
R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874  
R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126  
R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948  
R-NT2RP2003339//ESTs//1.3e-85:441:96//Hs.24115:N32618  
R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825  
R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014  
R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476  
R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502  
R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249

R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683

R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [*Canis familiaris*]//1.2e-106:508:98//Hs.131840:AI016073

R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//5.6e-21:161:70//Hs.43153:N22360

R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [*C.elegans*]//6.0e-105:529:96//Hs.8055:W60903

R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332

R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121

R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [*D.melanogaster*]//7.0e-71:365:95//Hs.101056:R52777

R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [*S.cerevisiae*]//2.3e-115:577:96//Hs.16277:N36831

R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733

R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270

R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783

R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170

R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101

R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684

R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//1.8e-58:316:94//Hs.28891:W72439

R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696

R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719

R-NT2RP2003596//ESTs, Weakly similar to No definition line found [*C.elegans*]//4.7e-101:495:98//Hs.34627:AA126463

R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067



R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981  
R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN  
MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188  
R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951  
R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523  
R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62/  
/Hs.65539:AI148540  
R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.  
norvegicus]//4.3e-99:492:96//Hs.93332:AA811920  
R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246  
R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4  
e-47:265:93//Hs.78494:AB011097  
R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401  
R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003  
R-ntnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//  
Hs.2384:U18914  
R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2  
-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577  
R-NT2RP2003751  
R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808  
R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709  
R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606  
R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds/  
/6.0e-106:531:96//Hs.90436:AF047437  
R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811  
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836  
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955  
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077  
R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838

R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124  
 R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167  
 R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341  
 R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611  
 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278  
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458  
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916  
 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347  
 R-NT2RP2003984  
 R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087  
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens] //3.2e-110:519:99//Hs.36093:AI149968  
 R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478  
 R-NT2RP2004041  
 R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706  
 R-NNNNNNNNNNNN//ESTs//1.4e-110:559:96//Hs.71916:AA219699  
 R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204  
 R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461  
 R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036  
 R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500  
 R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241  
 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Ant hocidaris crassispina] //1.0e-118:583:97//Hs.16520:AI224533  
 R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544  
 R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974

R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589  
 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167  
 R-NT2RP2004196  
 R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756  
 R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972  
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens] /  
 /5.2e-105:499:98//Hs.143460:AA483305  
 R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116  
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cd  
 s//3.4e-103:530:93//Hs.54900:AF039687  
 R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483  
 R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744  
 R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187  
 R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056  
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete c  
 ds//4.7e-110:544:96//Hs.61152:AF000416  
 R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788  
 R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223  
 R-NT2RP2004347  
 R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173  
 R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310  
 R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624  
 R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192  
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN FO  
 9G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:108:82//Hs.304  
 90:AA146916  
 R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646  
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473  
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900

R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921  
 R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121  
 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124  
 R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695  
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase  
 -1 (PKD1) mRNA, complete cds//8.6e-34:143:98//Hs.154729:AF017995  
 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700  
 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320  
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081  
 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347  
 R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470  
 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661  
 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126  
 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666  
 R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862  
 R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//4.5e-07:149:76//Hs.12845:N28835  
 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587  
 :96//Hs.5198:AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9  
 e-107:520:96//Hs.29956:AB007929  
 R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930  
 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0  
 e-120:600:96//Hs.154919:AB014525  
 R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793  
 R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433  
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.

3e-118:594:96//Hs.4236:AB007947

R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015

R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423

R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774

R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013

R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//8.0e-116:564:96//Hs.40820:AF058953

R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579

R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:AF054179

R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906

R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803

R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567

R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529

R-nnnnnnnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543

R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941

R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458

R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087

R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496

R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910

R-NT2RP2004985

R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902

R-NT2RP2005000

R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:AB014515

R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235

R-nnnnnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161  
 R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507  
 R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887  
 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220  
 R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757  
 R-NT2RP2005108  
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7  
 e-105:518:97//Hs.22616:AB014564  
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box  
 protein)//4.6e-69:464:85//Hs.100555:X98743  
 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383  
 R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180:AI341261  
 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744  
 R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438  
 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582  
 R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648  
 R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//2.4e  
 -101:513:95//Hs.155218:AJ007509  
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 H  
 OMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166  
 R-NT2RP2005227//Homo sapiens LIM protein mRNA, complete cds//1.0e-45:359  
 :82//Hs.154103:AF061258  
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Sacc  
 haromyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587  
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503  
 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK  
 637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.230  
 47:N66596  
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272

R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001  
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219  
R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590  
R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261  
R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338  
R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701  
R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699  
R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445  
R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544  
R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247  
R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304  
R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697  
R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B04 95.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631  
R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068  
R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423  
R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096  
R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307  
R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936  
R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019  
R-NT2RP2005476//ESTs//5.1e-40:205:98//Hs.101577:AI168526  
R-NT2RP2005490//ESTs//1.3e-70:364:96//Hs.134382:AA083573  
R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455

R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540  
R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426  
R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD  
REGULATORY SUBUNIT, NEURONAL ISOFORM [*Oryctolagus cuniculus*]//2.3e-45:2  
84:88//Hs.85752:AI138993  
R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755  
R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C1  
2C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.  
5298:AA725071  
R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mR  
NA, complete cds//3.2e-110:570:94//Hs.119023:AF092563  
R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING EN  
TRY !!!! [H.sapiens]//1.3e-84:433:95//Hs.36942:AA524535  
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856  
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e  
-108:560:94//Hs.159597:AJ012449  
R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.  
7e-115:583:96//Hs.62515:AB007963  
R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572  
R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567  
R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169  
R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240  
R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733  
R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060  
R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788  
R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229  
R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211  
R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740  
R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173



R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis]//  
2.9e-103:525:96//Hs.70589:AA868470

R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:6  
0//Hs.162:X16302

R-NT2RP2005669//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//2.7e  
-14:87:100//Hs.146406:AF069987

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, co  
mplete cds//5.8e-91:434:98//Hs.25664:AF089814

R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229

R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236

R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643

R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tau  
rus]//2.8e-68:376:93//Hs.9095:AA532630

R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3  
e-105:503:98//Hs.61638:AB018342

R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precu  
sor [H.sapiens]//5.4e-105:500:98//Hs.14298:AI417523

R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982

R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455

R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153

R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258

R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064

R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, c  
omplete cds//4.3e-42:223:96//Hs.159651:AF068868

R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, comple  
te cds//1.2e-104:494:98//Hs.26285:AF082516

R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163

R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463

R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTA

SE [Homo sapiens] //5.4e-112:559:96//Hs.14214:AI189379  
R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa] //3.0e-108:544:96//Hs.22151:AI214321  
R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664  
R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724  
R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398  
R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746  
R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981  
R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122  
R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403  
R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062  
R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462  
R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105  
R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133  
R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315  
R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268  
R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans] //2.4e-73:397:94//Hs.16667:T92427  
R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus] //2.8e-114:560:97//Hs.9082:AA873170  
R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419  
R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988  
R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080  
R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347  
R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans] //1.2e-50:278:94//Hs.7194:AI185631  
R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492  
R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714

R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093  
R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918  
R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA  
, complete cds//0.031:254:62//Hs.46440:U21943  
R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365  
R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522  
R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255  
:72//Hs.154103:AF061258  
R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435  
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1  
e-110:553:95//Hs.109299:AB014554  
R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.15129  
3:U79276  
R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398  
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153  
910:X96484  
R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312  
R-NT2RP2006238//ESTs, Highly similar to ra8 [R.norvegicus]//1.5e-29:183:  
91//Hs.4048:AA404253  
R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928  
R-NT2RP2006261//ESTs//3.4e-57:326:92//Hs.22523:W02999  
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:4  
81:97//Hs.3404:AF035262  
R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015  
R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapien  
s]//1.9e-89:460:96//Hs.21889:N78664  
R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771  
R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412  
R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321

R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411

R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053

R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.115325:D84488

R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092

R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146

R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266

R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478

R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679

R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947

R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474

R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886

R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

R-NNNNNNNNNNNN//ESTs//2.0e-112:533:98//Hs.18685:AI393829

R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112

R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972

R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219

R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213

R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202

R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095

R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574

R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029  
 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715  
 R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241  
 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000  
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2  
 e-116:578:96//Hs.13273:AB011164  
 R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418  
 R-NT2RP3000186  
 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882  
 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091  
 R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306  
 R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817  
 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819  
 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239  
 R-NT2RP3000251  
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:  
 532:97//Hs.111086:AI379177  
 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073  
 R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446  
 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sa  
 piens]//3.6e-103:516:96//Hs.4894:AI191323  
 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117  
 R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438  
 R-NT2RP3000324  
 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267  
 R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689  
 R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225  
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:  
 556:96//Hs.111086:AI379177

R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741  
 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S  
 .cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423  
 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303  
 R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106  
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cd  
 s//4.2e-111:529:98//Hs.28307:AF071185  
 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947  
 R-NT2RP3000433  
 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340  
 R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254  
 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102  
 R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492  
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragm  
 ent//1.8e-23:347:70//Hs.114963:L34408  
 R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600  
 R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141  
 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667  
 R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151  
 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161  
 R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.  
 95:85:71//Hs.5184:AA709151  
 R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180  
 R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036  
 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68/  
 /Hs.79077:D87071  
 R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447  
 R-NT2RP3000582//ESTs//2.1e-25:131:80//Hs.152465:AA563785  
 R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511

R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817  
R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916  
R-nnnnnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312  
R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880  
R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049  
R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394  
R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739  
R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315  
R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA719022  
R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084  
R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185  
R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185  
R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873  
R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.146589:AI085578  
R-NT2RP3000736  
R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960  
R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447  
R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243  
R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583  
R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810  
R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582  
R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081  
R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082

R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022  
 R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI051657  
 R-NT2RP3000850  
 R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272  
 R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895  
 R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741  
 R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837  
 R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673  
 R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468  
 R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217  
 R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385  
 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus] /  
 /9.5e-113:566:96//Hs.5900:AA035728  
 R-NT2RP3000919  
 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.5e-25:375:71//Hs.2953:X844  
 07  
 R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178  
 R-NT2RP3000994//ESTs//3.5e-111:537:97//Hs.21146:AA683542  
 R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405  
 R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029  
 R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044  
 R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo  
 sapiens] //5.6e-102:486:99//Hs.145956:AA007349  
 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.00  
 12:447:58//Hs.2133:U18991  
 R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874  
 R-NT2RP3001096//ESTs//1.1e-110:540:96//Hs.42824:AA873182  
 R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832  
 R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325



R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster] //3.2e-104:543:95//Hs.93796:C06063

R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575

R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878

R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779

R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180

R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166

R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188

R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761

R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305

R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //9.6e-113:552:97//Hs.23900:U82984

R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717

R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266

R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460

R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139

R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963

R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196

R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399

R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens] //2.8e-89:462:95//Hs.116793:AA779588

R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus] //5.2e-82:466:91//Hs.66048:AA524416

R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631

R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997

R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135

R-NT2RP3001268//Human Aac11 (aac11) mRNA, complete cds//0.12:494:59//Hs.

151031:U83857

R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965

R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.113184:N25651

R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332

R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691

R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571

R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989

R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete  
cds//0.22:199:63//Hs.159534:U35234

R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.  
9e-114:566:96//Hs.18586:AB007920

R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653

R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798

R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090

R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778

R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP  
95 [R.norvegicus]//5.7e-92:522:90//Hs.96200:AA218942

R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375

R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232

R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628

R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186

R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898

R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817

R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94/  
/Hs.6957:AF052158

R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692

R-nnnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:  
533:91//Hs.85844:X66397

R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374

R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560

R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994

R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs  
.155464:AF088219

R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658

R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280

R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009

R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783

R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-  
61:338:93//Hs.519:U13395

R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (T  
RC8) mRNA, complete cds//6.8e-112:549:97//Hs.28285:AF064801

R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047

R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-5  
9:427:83//Hs.5247:AF029750

R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463

R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus  
]//2.8e-76:392:95//Hs.66048:AA524416

R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477

R-NT2RP3001587//Homo sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:8  
6:88//Hs.4311:AB015337

R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194

R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328

R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798

R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598

R-NT2RP3001629

R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:  
541:96//Hs.9899:AF099149

R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989  
 R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709  
 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030  
 R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189  
 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648  
 R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225  
 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558  
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:8  
 7//Hs.40100:AB002390  
 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312  
 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618  
 R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669  
 R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR  
 ECURSOR [Mus musculus]//4.1e-80:444:91//Hs.6823:W18181  
 R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099  
 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923  
 R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810  
 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440  
 R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968  
 R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.  
 sapiens]//1.2e-87:450:96//Hs.20281:N92517  
 R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725  
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2  
 e-113:549:97//Hs.28169:AB007928  
 R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:11  
 9:99//Hs.44268:AA455900  
 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X759  
 62  
 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292

R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117  
 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900  
 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792  
 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642  
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180  
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666  
 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]  
 ]//1.0e-40:202:100//Hs.24709:AI123300  
 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781  
 R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737  
 R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1  
 [Saccharomyces cerevisiae]//1.3e-95:483:96//Hs.5771:W74591  
 R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990  
 R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325  
 R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889  
 R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310  
 :99//Hs.11449:AI201540  
 R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088  
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087  
 :X86779  
 R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729  
 R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs  
 .155464:AF088219  
 R-NT2RP3002033  
 R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081  
 R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426  
 R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI365221  
 R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66/  
 /Hs.90438:D63486

R-NT2RP3002062

R-nnnnnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657

R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139

R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148

R-NT2RP3002102

R-NT2RP3002108

R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385

R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:AI249703

R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEI

N 1 HOMOLOG [Homo sapiens] //6.2e-107:534:96//Hs.59523:AA602837

R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293

R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024

R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713

R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120

R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598

R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446

R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588

R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672

R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743

R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171

R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898

R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500

R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN

1 HOMOLOG [H.sapiens] //1.8e-19:136:87//Hs.106928:AI041737

R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667

R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0

048:221:64//Hs.556:L41887

R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A)

gene//5.8e-105:516:94//Hs.6483:Y16355

R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5  
e-103:524:95//Hs.12707:AB014578

R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0  
.54:108:71//Hs.28914:Y00486

R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185

R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R10  
7.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436

R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTI  
NG-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:49  
7:96//Hs.6650:AA843246

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1:1  
e-83:438:94//Hs.19542:AB018272

R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673

R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3)  
mRNA, complete cds//0.14:184:63//Hs.89230:AF031815

R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78  
//Hs.129883:AB007880

R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850

R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100/  
/Hs.76691:AF070673

R-NT2RP3002603

R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365

R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573

R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172

R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila  
melanogaster]//5.9e-109:537:97//Hs.19348:AA151678

R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502

R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871

R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//5.0e-101:524:95//Hs.32580:AI123601  
 R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169  
 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945  
 R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159  
 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973  
 R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958  
 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377  
 R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240  
 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080  
 R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678  
 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641  
 R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262  
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2  
 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5  
 e-110:570:95//Hs.6162:AB018314  
 R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286  
 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975  
 R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698  
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0492//0.23:563:56//Hs.127338:AB007961  
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGAS  
 E 1 [Saccharomyces cerevisiae]//2.0e-56:387:86//Hs.144597:W20143  
 R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850  
 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116  
 R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553  
 R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423  
 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTE



IN [Mus musculus] //3.0e-100:528:94//Hs.90353:N98551  
R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355  
R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912  
R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans] //5.9e-83:392:9  
9//Hs.101364:AA534439  
R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809  
R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466  
R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441  
R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520  
R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982  
R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus  
musculus] //3.3e-107:535:96//Hs.27437:AA004208  
R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632  
R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774  
R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007  
R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226  
R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944  
R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796  
R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634  
R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573  
R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107  
R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoide  
um] //2.0e-40:229:93//Hs.17377:AI078151  
R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343  
R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628  
R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960  
R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061  
R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:  
550:93//Hs.11702:L36983

R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035  
 R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055  
 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818  
 R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261  
 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931  
 R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445  
 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289  
 R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993  
 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102  
 R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155  
 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567  
 R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272  
 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721  
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM  
 OLOG [H.sapiens]//2.2e-24:418:67//Hs.139488:AI124095  
 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372  
 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041  
 R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023  
 R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156  
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete c  
 ds//3.6e-97:479:96//Hs.14934:AF004828  
 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1  
 e-102:527:93//Hs.26450:AB018268  
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.eleg  
 ans]//4.0e-106:549:94//Hs.7886:AI057529  
 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U025  
 56  
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRN  
 A//4.1e-33:217:88//Hs.8068:U00952

R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430  
 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681  
 R-NT2RP3003564  
 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721  
 R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944  
 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759  
 R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448  
 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//  
 Hs.17217:U49957  
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310  
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714  
 R-NT2RP3003672  
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036  
 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768  
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923  
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.  
 6e-103:492:97//Hs.48513:AB018300  
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863  
 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747  
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913  
 R-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC//8.9e-108:551  
 :95//Hs.115742:AF077754  
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446  
 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidoca  
 ldarius]//3.4e-89:456:95//Hs.5555:AI285198  
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627  
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761  
 R-NT2RP3003828//ESTs, Weakly similar to unknown [H.sapiens]//9.6e-98:511  
 :95//Hs.26955:AI333224

R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743  
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611  
 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888  
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298  
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170  
 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726  
 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933  
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221  
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409  
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593  
 R-NT2RP3004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142  
 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714  
 R-NT2RP3004041  
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820  
 R-NT2RP3004070//ESTs//5.5e-108:552:95//Hs.23392:AI310139  
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W45387  
 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104  
 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045  
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092  
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696  
 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334  
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425  
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093  
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126  
 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41

:266:89//Hs.6314:AA522619

R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe] //3.7e-112:547:97//Hs.99819:AI346680

R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794

R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252

R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827

R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628

R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens] //1.6e-89:468:95//Hs.5117:AA831530

R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623

R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630

R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264

R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258

R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223

R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044

R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224

R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans] //0.30:253:58//Hs.97184:AA385934

R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985

R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621

R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917

R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616

R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332

R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406

R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925

R-NT2RP3004480  
R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504  
R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens] //3.4e-100:508:95//Hs.47393:AA218858  
R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735  
R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus] //1.8e-83:465:92//Hs.137064:AA318257  
R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971  
R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865  
R-nnnnnnnnnnnnn  
R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232  
R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461  
R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674  
R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493  
R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456  
R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213  
R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157  
R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723  
R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680  
R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335  
R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560  
R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219  
R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266  
R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens] //8.3e-98:462:99//Hs.10114:AI345945

R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030  
R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287  
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538  
R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:AB007952  
R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014  
R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294  
R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436  
R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295  
R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569  
R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257  
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:AB014600  
R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788  
R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390  
R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185  
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP10)//2.9e-70:354:96//Hs.155481:AJ006470  
R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757  
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:AF091092  
R-NT2RP4000263  
R-ntnnnnnnnnnnnn//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104:525:96//Hs.152069:AA548972  
R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631

R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99/  
/Hs.13410:AF070524

R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760

R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390

R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.  
6e-111:520:99//Hs.107479:AB018281

R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-110:527:98//Hs.31323:AF044195

R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130

R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498

R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376

R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk3  
0b3.5 [C.elegans]//3.9e-87:499:91//Hs.26156:AA630975

R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN  
IN RPS7A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:46  
8:96//Hs.93871:AI191318

R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011

R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955

R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953

R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783

R-nt2rp4000455//ESTs//4.5e-89:455:96//Hs.62638:AA127740

R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167

R-nt2rp4000480

R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05  
D3.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:AI424792

R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713

R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U1086



R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874  
 R-NT2RP4000519  
 R-NT2RP4000524//ESTs, Highly similar to rsec8 [R.norvegicus] //3.4e-93:49  
 6:93//Hs.107394:H07126  
 R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213  
 R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328  
 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.nor  
 vegicus] //8.2e-92:448:98//Hs.25597:H93026  
 R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840  
 R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263  
 R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531  
 R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393  
 R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704  
 R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651  
 R-NT2RP4000724//ESTs//1.5e-83:442:94//Hs.142114:AA205615  
 R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399  
 R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211  
 R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312  
 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.  
 1e-106:550:94//Hs.25132:AB007939  
 R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834  
 R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028  
 R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104  
 R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356  
 R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185  
 R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617  
 R-nnnnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594  
 R-nnnnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106  
 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens] //5.9e-17:13

4:85//Hs.14146:W92235  
R-nnnnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683  
R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,  
partial cds//8.2e-108:548:95//Hs.24812:AF069532  
R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905  
R-NT2RP4000955//ESTs//3.5e-10:119:78//Hs.42946:N21111  
R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986  
R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179  
R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017  
R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98/  
/Hs.12457:AF052123  
R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018  
R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620  
R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp  
lete cds//1.1e-28:439:68//Hs.129735:AF010144  
R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769  
R-NT2RP4001006//ESTs, Moderately similar to ORF2: function unknown [H.sa  
piens]//6.6e-124:574:99//Hs.47393:AA218858  
R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635  
R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292  
R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLA  
SMIC [Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA088424  
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94/  
/Hs.100955:AB007859  
R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:  
485:99//Hs.10114:AI345945  
R-NT2RP4001078  
R-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase,  
partial//1.7e-119:569:98//Hs.106778:AJ010953

R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668

R-nnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164

R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055

R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617

R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737

R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357

R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476

R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890

R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [*Saccharomyces cerevisiae*]//5.4e-113:573:96//Hs.5249:U55977

R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453

R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171

R-NT2RP4001150//ESTs//1.9e-90:422:100//Hs.125490:AI138884

R-NT2RP4001159

R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278

R-nnnnnnnnnnnnnn//ESTs//1.1e-25:140:97//Hs.83756:AI002822

R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514

R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495

R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [*Homo sapiens*]//4.4e-123:624:95//Hs.22744:AI379892

R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750

R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103

R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120

R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255

R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430

R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933

R-nnnnnnnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588

R-NT2RP4001313  
 R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892  
 R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612  
 R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732  
 R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837  
 R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616  
 R-NT2RP4001372  
 R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN  
 TRK2-MRS4 INTERGENIC REGION [*Saccharomyces cerevisiae*]//1.7e-108:546:96/  
 /Hs.32271:AA203680  
 R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299  
 R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501  
 R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN  
 PAP1-MRPL13 INTERGENIC REGION [*Saccharomyces cerevisiae*]//3.8e-79:438:9  
 3//Hs.21938:W81045  
 R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132  
 R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649  
 R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [*H.sapiens*]//1.6e  
 -102:498:97//Hs.62386:AA512948  
 R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433  
 R-NT2RP4001447  
 R-NT2RP4001474  
 R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655  
 R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846  
 R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511  
 R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385  
 R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [*C.elegans*]//2.9e-107:5  
 46:96//Hs.5570:AI377863  
 R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292

R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C  
HAIN 5 [*Paramecium tetraurelia*]//2.8e-120:566:98//Hs.108530:AA523928  
R-nnnnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68  
[*S.cerevisiae*]//1.4e-26:184:88//Hs.136189:AA133224  
R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552  
R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285  
R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437  
R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251  
R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906  
R-NT2RP4001575  
R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOC  
HONDRIAL [*S.cerevisiae*]//8.7e-112:557:97//Hs.7558:AA526812  
R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776  
R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657  
R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737  
R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e  
-116:559:97//Hs.5332:AF007151  
R-NT2RP4001644//ESTs, Moderately similar to MNK1 [*H.sapiens*]//5.3e-36:19  
2:97//Hs.5662:AA868361  
R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R  
06F6.2 IN CHROMOSOME II [*Caenorhabditis elegans*]//1.1e-104:525:96//Hs.20  
472:W28734  
R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805  
R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete seque  
nce//5.7e-118:583:96//Hs.15562:U96629  
R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941  
R-nnnnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSY  
LTRANSFERASE PRECURSOR [*D.melanogaster*]//3.4e-73:362:97//Hs.152332:A1141  
922

R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692  
 R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:  
 X78926  
 R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315  
 R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien  
 s]//2.0e-62:326:94//Hs.110839:W28098  
 R-NT2RP4001803  
 R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133  
 R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434  
 R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826  
 R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663  
 R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210  
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:8  
 8//Hs.154326:D42087  
 R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602  
 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528  
 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606  
 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099  
 R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848  
 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436  
 R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793  
 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73  
 919:X81637  
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanog  
 aster]//8.3e-87:457:94//Hs.41793:AA775879  
 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252  
 R-NT2RP4002018  
 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseud  
 omonas fluorescens]//4.7e-09:90:86//Hs.41127:AA555184

R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738  
 R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106  
 R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679  
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198  
 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sa  
 piens] //1.6e-61:464:82//Hs.144228:N99507  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN CO  
 8B11.3 IN CHROMOSOME II [C.elegans] //2.3e-56:271:100//Hs.6185:AA428565  
 R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407  
 R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592  
 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555  
 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen n  
 ecrosis virus] //1.9e-65:373:92//Hs.31532:H18272  
 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090  
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8  
 e-115:605:94//Hs.108258:AB007934  
 R-OVARC1000004  
 R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929  
 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635  
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273  
 R-OVARC1000017  
 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286  
 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-4  
 6:331:83//Hs.96247:X95073  
 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041  
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367  
 R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R67871  
 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL0312

R-nnnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703  
R-OVARC1000091//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens] /  
/3.9e-112:596:94//Hs.20597:W58370  
R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942  
R-OVARC1000106  
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48  
-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250  
R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:48  
9:74//Hs.101238:Y11312  
R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482  
R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214  
R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090  
R-OVARC1000151  
R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023  
R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629  
R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339  
:81//Hs.154103:AF061258  
R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sa  
piens] //1.1e-32:196:92//Hs.64322:AA142864  
R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874  
R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958  
R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130  
R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN  
CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae] //3.3e-74:403:93  
//Hs.108117:AI097079  
R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476  
R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MO  
V10 [Mus musculus] //2.9e-37:191:98//Hs.20725:AI027777  
R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449



R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743  
 R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptid  
 e 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682  
 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863  
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672  
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423  
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928  
 R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219  
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211  
 :79//Hs.108287:L27670  
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237  
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034  
 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426  
 R-OVARC1000437  
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671  
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA,  
 complete cds//4.3e-45:320:84//Hs.73614:U83460  
 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.  
 6e-79:418:94//Hs.12334:AB014583  
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582  
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576  
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211  
 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926  
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:  
 514:96//Hs.11833:AI299947  
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983  
 R-OVARC1000496  
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484  
 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs

.155464:AF088219

R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248

R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021

R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106

R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285

R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587

R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627

R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219

R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053

R-OVARC1000605

R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA 0501//6.4e-47:417:77//Hs.159897:AB007970

R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:AB011162

R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480

R-nnnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522

R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875

R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517

R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901

R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461

R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736

R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918  
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF  
 -2 alpha kinase [D.melanogaster] //4.6e-28:430:69//Hs.42457:AA523306  
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016  
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793  
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659  
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:9  
 5//Hs.3069:L11066  
 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764  
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.  
 2e-106:536:95//Hs.61628:Y17711  
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73  
 919:X81637  
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//H  
 s.18910:AF045584  
 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096  
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674  
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292  
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN  
 ROCC-PTA INTERGENIC REGION [Bacillus subtilis] //7.9e-98:525:93//Hs.10366  
 :W21953  
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777  
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401  
 R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350  
 R-OVARC1000912  
 R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814  
 R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127  
 R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696  
 R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215

R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794  
R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971  
R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs  
.155464:AF088219  
R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80/  
/Hs.43681:AL022394  
R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909  
R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.eleg  
ans] //3.5e-68:346:96//Hs.25544:AA532784  
R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811  
R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73/  
/Hs.127649:AB007874  
R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448  
R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//  
1.7e-28:181:77//Hs.139107:K00629  
R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270  
R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117  
R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630  
R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apa  
f-1) mRNA, complete cds//2.1e-09:137:74//Hs.77579:AF013263  
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:  
501:96//Hs.9899:AF099149  
R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046  
R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384  
R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12  
962  
R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231  
R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652  
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial

cds//7.3e-97:463:98//Hs.3426:AF082657  
 R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844  
 R-OVARC1001074  
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//  
 Hs.103126:U57029  
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone I  
 MAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berl  
 in))//1.4e-96:325:98//Hs.21753:AJ005897  
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.  
 3e-75:386:95//Hs.26584:AF051782  
 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete  
 cds//3.9e-37:283:84//Hs.46468:U45984  
 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548  
 R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312  
 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN  
 G ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226  
 R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223  
 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727  
 R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200  
 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs  
 .155464:AF088219  
 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223  
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA,  
 complete cds//6.6e-64:247:80//Hs.97203:U83171  
 R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343  
 R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826  
 R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025  
 R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668  
 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166  
 R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929  
 R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708  
 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532  
 R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113  
 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8  
 e-70:334:100//Hs.23763:AB011090  
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73  
 919:X81637  
 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1  
 .0:147:63//Hs.76494:U41344  
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs  
 .155464:AF088219  
 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNIN  
 G ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356  
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67  
 247  
 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216  
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90  
 657  
 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844  
 R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777  
 R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415  
 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.  
 1e-53:344:72//Hs.153468:AB011147  
 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958  
 R-OVARC1001391  
 R-nnnnnnnnnnnnn//ESTs//0.0039:48:95//Hs.117964:N20913

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//  
Hs.21586:AB006651

R-OVARC1001419

R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136

R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427

R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345

R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592

R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700

R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694

R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete  
cds//3.0e-117:585:96//Hs.6534:AF016507

R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs  
.155464:AF088219

R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//H  
s.6396:AB016492

R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388

R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA/  
/4.4e-20:150:89//Hs.155160:AF031166

R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:7  
2//Hs.154326:D42087

R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019

R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965

R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78/  
/Hs.5158:AB007869

R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659

R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854

R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080

R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784  
R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [*Xenopus laevis*]  
//1.2e-27:236:81//Hs.15485:AA046954  
R-OVARC1001731//Tropomyosin 4 (fibroblast)//7.9e-74:422:90//Hs.102824:XO  
5276  
R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.  
7e-62:300:83//Hs.144563:AF057280  
R-nnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [*S.cerevisiae*]  
//6.8e-100:540:92//Hs.117741:AA903456  
R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3,  
p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.155377:U97670  
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.  
0e-109:529:97//Hs.15869:AB014575  
R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127  
R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604  
R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978  
R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81/  
/Hs.153563:AF011333  
R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688  
R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831  
R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1  
e-15:519:63//Hs.25639:AB011110  
R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705  
R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621  
R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160  
R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809  
R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-  
105:571:91//Hs.25300:AF070611  
R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476



R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.  
2e-49:302:90//Hs.153468:AB011147

R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749

R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842

R-OVARC1001928

R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [*S.cerevisiae*] //2.5e-39:253:88//Hs.117741:AA903456

R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [*Homo sapiens*] //8.3e-96:498:94//Hs.22744:AI379892

R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875

R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729

R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887

R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531

R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934

R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556

R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315

R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860

R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130

R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [*Caenorhabditis elegans*] //1.7e-102:485:98//Hs.137516:AA805691

R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825

R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923  
 R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631  
 R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160  
 R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478  
 R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337  
 R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920  
 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557  
 R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223  
 R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870  
 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440  
 R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503  
 R-PLACE1000050//ESTs//9.7e-90:453:96//Hs.27410:N25612  
 R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499  
 R-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-61:331:94//Hs.30026:AI356771  
 R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659  
 R-PLACE1000081  
 R-PLACE1000094  
 R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505  
 R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:94//Hs.9670:AA632135  
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291  
 R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]//2.0e-19:114:95//Hs.7036:W22072  
 R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946

R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916

R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U  
17077

R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545

R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912

R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940

R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424

R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126

R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994

R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708

R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959

R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089

R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799

R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125

R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131

R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long fo  
rm (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456

R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb pr  
ecursor [H.sapiens]//2.0e-58:410:81//Hs.97579:AA398118

R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793

R-PLACE1000481//ESTs, Weakly similar to Ndr protein kinase [H.sapiens]//  
3.2e-109:549:95//Hs.19074:U69566

R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog  
r-vps33b [R.norvegicus]//3.5e-83:435:94//Hs.26510:AA700425

R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729

R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2  
e-32:208:88//Hs.153026:AB014540

R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN  
IXR1-TFA1 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//

Hs.163791:W25348

R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:AI380485

R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353

R-nnnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542

R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030

R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087

R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301

R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308

R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone I MAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896

R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353

R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485

R-PLACE1000716

R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701

R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396

R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [C.elegans]//3.9e-40:224:94//Hs.87889:AA262008

R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548

R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482

R-nnnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.2014  
4:AF088219

R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189

R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory pr  
oteins [H.sapiens] //7.7e-31:220:86//Hs.117576:R33135

R-nnnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588

R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039

R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN  
YHR148W [Saccharomyces cerevisiae] //2.2e-92:467:95//Hs.6118:AI141558

R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846

R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091

R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697

R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941

R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689

R-PLACE1000979

R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725

R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens] //5.2e-63:34  
3:93//Hs.5662:AA868361

R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146

R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878

R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736

R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762

R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120

R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124

R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580

R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259  
:59//Hs.31575:AF100141

R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268

R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610

R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594  
R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834  
R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H. sapiens] //0.91:77:71//Hs.115211:AA287527  
R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297  
R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus] //1.9e-99:512:94//Hs.24884:AA176812  
R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464  
R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131  
R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371  
R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780  
R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460  
R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus] //2.7e-22:181:84//Hs.48320:AA149548  
R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens] //4.2e-34:195:92//Hs.86276:W27601  
R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056  
R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160  
R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077  
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219  
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615  
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030  
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419  
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555  
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348  
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//  
 2.6e-45:242:95//Hs.110404:AF091087  
 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800  
 R-PLACE1001440  
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115  
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547  
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625  
 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617  
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361  
 R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds//2.1e-57:339:90//H  
 s.4742:AB006969  
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153  
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265  
 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431  
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249  
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601  
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904  
 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683  
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1  
 e-42:217:97//Hs.75258:AF054174  
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sa  
 piens]//1.5e-78:458:91//Hs.114547:AA167095  
 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526  
 R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640  
 R-PLACE1001672//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
 ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804

R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250

R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124

R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903

R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667

R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993

R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171

R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113

R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266

R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479

R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937

R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243

R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662

R-PLACE1001761

R-PLACE1001771//ESTs//0.92:165:62//Hs.47387:N51980

R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236

R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//1.3e-93:463:95//Hs.40820:AF058953

R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219

R-PLACE1001845

R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868

R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009

R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936



R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.

85:130:66//Hs.151406:AB014523

R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941

R-PLACE1002046

R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595

R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094

R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619

R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552

R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632

R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311

R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293

R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937

R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614

R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMO

LOG [H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189

R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965

R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745

R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793

R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788

R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892

R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257

R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8

e-67:501:81//Hs.23094:M19503

R-PLACE1002319//ESTs//1.4e-28:178:92//Hs.7353:AA209308

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6

e-95:501:93//Hs.18277:AB018271

R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291

R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381

R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959  
R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110  
R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60  
//Hs.83715:X69804  
R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333  
R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320  
R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:16  
6:85//Hs.19368:U69263  
R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132  
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STA  
M2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273  
R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429  
R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83/  
/Hs.5158:AB007869  
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING E  
NTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609  
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1  
e-88:582:85//Hs.88756:AB018256  
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19  
:116:93//Hs.99348:AC004774  
R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491  
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosoph  
ila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437  
R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131  
R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738  
R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778  
R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus inf  
luenzae]//1.2e-44:228:97//Hs.7527:AA843208  
R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147

R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749  
R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)  
//1.0:189:58//Hs.75703:J04130  
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternativ  
ely spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180  
R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830  
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled recep  
tor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586  
R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865  
R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099  
R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014  
R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593  
R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955  
R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392  
R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916  
R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sa  
piens]//2.1e-42:233:94//Hs.61518:AA167094  
R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142  
R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756  
R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539  
R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762  
R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332  
R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995  
R-PLACE1002962  
R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202  
R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941  
R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING EN  
TRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268  
R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268

R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499  
 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156:60//  
 Hs.82042:D87075  
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840  
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777  
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.6318:AI131178  
 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359  
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//  
 Hs.49346:U51920  
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757  
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467  
 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924  
 R-PLACE1003176  
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453  
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017  
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802  
 R-PLACE1003238//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:43  
 6:94//Hs.58561:W79123  
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460  
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131  
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326  
 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986  
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993  
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !

!!! [H.sapiens] //3.3e-94:463:97//Hs.155050:AA908765  
R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438  
R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701  
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715  
R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636  
R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234  
R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans] //3.5e-18:109:95//Hs.27670:AI051591  
R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941  
R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909  
R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755  
R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020  
R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840  
R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697  
R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671  
R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270  
R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952  
R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505  
R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980  
R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461  
R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens] //7.4e-69:338:98//Hs.110439:N93209  
R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321  
R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591  
R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956  
R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapie

ns]//1.5e-14:264:65//Hs.158253:R86178  
R-PLACE1003584  
R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542  
R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5  
.8e-75:459:89//Hs.23884:AI377106  
R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875  
R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88/  
/Hs.56851:D83200  
R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299  
R-nnnnnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446  
R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943  
R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285  
R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247  
R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607  
R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521  
R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866  
R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639  
R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987  
R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087  
R-PLACE1003760//Human globin gene//1.9e-98:538:91//Hs.100090:M69023  
R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512  
R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302  
:U88965  
R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798  
R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199  
:97//Hs.115197:AA215757  
R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909  
R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.  
2e-36:236:88//Hs.153468:AB011147

R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
 G ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092  
 R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059  
 R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058  
 R-PLACE1003864  
 R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871  
 R-oooooooooooooooo  
 R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595  
 R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915  
 R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259  
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.  
 5e-54:282:96//Hs.58553:AA100804  
 R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760  
 R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236  
 R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110  
 R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567  
 R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330  
 R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231  
 R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052  
 R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770  
 R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244  
 R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714  
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:49  
 1:76//Hs.113283:AF018080  
 R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601  
 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11  
 (COX11) mRNA, complete cds//4.7e-78:434:91//Hs.153504:AF044321  
 R-PLACE1004197  
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precur

sor, mRNA, complete cds//1.5e-105:501:98//Hs.24640:AF069493  
 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952  
 R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630  
 R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209  
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:  
 J00124  
 R-PLACE1004270//ESTs//0.011:264:59//Hs.110044:AA181800  
 R-PLACE1004274//Human retinoic acid receptor-beta associated open readin  
 g frame, complete sequence//0.28:121:66//Hs.1938:S82362  
 R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c  
 omplete cds//1.4e-107:581:91//Hs.127007:AF084830  
 R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114  
 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//2.9e-28:279:77//Hs.38687:AA744496  
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cere  
 visiae]//8.2e-61:313:95//Hs.71435:AI253099  
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:  
 590:94//Hs.11171:Y11588  
 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducibl  
 e), polypeptide 2//6.7e-69:572:77//Hs.1361:M55053  
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1-  
 mRNA, complete cds//7.7e-72:379:93//Hs.16232:AF100153  
 R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309  
 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556  
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-b  
 inding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000  
 R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467  
 R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665  
 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101



R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283

R-PLACE1004451

R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980

R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721

R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578

R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194

R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:278:61//Hs.89663:L13286

R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117

R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493

R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164

R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553

R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.115325:D84488

R-PLACE1004550

R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742

R-PLACE1004629//ESTs, Weakly similar to OS-9 precursor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181

R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903

R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734

R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257

R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.8e-90:510:91//Hs.80019:AF035606

R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482  
R-PLACE1004686  
R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552  
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374  
R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans] //3.4e-80:413:94//Hs.23528:AI279571  
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997  
R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N63911  
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619  
R-nnnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195  
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374  
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367  
R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548  
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178  
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856  
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250  
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356  
R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.73821:M35663  
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185  
R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299  
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901  
R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae] //6.5e-71:381:93//Hs.8383:AA013272  
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308

R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456

R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI281881

R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597

R-PLACE1004913//ESTs//4.5e-75:375:96//Hs.91115:AI221563

R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948

R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.17839:AF099936

R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980

R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166

R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013

R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106

R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789

R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776

R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335

R-PLACE1005026

R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719

R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147

R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605

R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103

R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985

R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080

R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364  
 R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99  
 :531:92//Hs.75437:L40401  
 R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336  
 R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.  
 2e-40:232:82//Hs.155344:U91985  
 R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225  
 R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423  
 R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349  
 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013  
 R-PLACE1005176//ESTs//5.4e-75:366:97//Hs.48119:AA454227  
 R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589  
 R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830  
 R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211  
 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532  
 R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767  
 R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524  
 R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633  
 R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516  
 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322  
 R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937  
 R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797  
 R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614  
 R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:  
 94//Hs.136309:AB007960  
 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343  
 R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442  
 :97//Hs.70202:AA732975  
 R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901

R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80/  
/Hs.43681:AL022394

R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978

R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304

R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423

R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3  
e-88:561:86//Hs.23094:M19503

R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e  
-80:549:83//Hs.78935:U29607

R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046

R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875

R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:  
319:59//Hs.62705:AB000220

R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cd  
s//5.4e-57:277:98//Hs.28307:AF071185

R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325

R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP  
)//8.9e-20:321:69//Hs.155481:AJ006470

R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325

R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K1  
2H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.381  
14:N62927

R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555

R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PRO  
TEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W8  
1261

R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835

R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612

R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023

R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927  
 R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857  
 R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964  
 R-PLACE1005630  
 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452  
 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete  
 cds//1.0e-111:585:93//Hs.8765:AF083255  
 R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169  
 R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2  
 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587  
 R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355  
 R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332  
 R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259  
 R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protei  
 n [M.musculus]//1.3e-42:236:94//Hs.23889:AI341137  
 R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070  
 R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:8  
 7//Hs.154326:D42087  
 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK  
 757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88:98//Hs.1098  
 57:AA088385  
 R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941  
 R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327  
 R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693  
 R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058  
 R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58/  
 /Hs.75770:L41870  
 R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965  
 R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471

R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305  
R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842  
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558  
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981  
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501  
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793  
R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8  
e-27:382:70//Hs.23094:M19503  
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:37  
7:93//Hs.5662:AA868361  
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142  
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913  
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729  
R-PLACE1005953  
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN  
CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88  
//Hs.108117:AI097079  
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239  
R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897  
R-PLACE1005990  
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:  
74//Hs.153014:AB002353  
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN  
APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:5  
93:93//Hs.111449:AI192946  
R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERAS  
E [D.melanogaster]//5.7e-100:596:88//Hs.24284:AA595596  
R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276  
R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:49

1:98//Hs.61164:AI096332  
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765  
R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
G ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314  
R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904  
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002  
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN  
SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:  
91//Hs.5249:U55977  
R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glyco  
gen debranching enzyme, glycogen storage disease type III)//0.038:463:59  
//Hs.904:U84010  
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886  
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925  
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128  
R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:9  
4//Hs.152894:AC005239  
R-nnnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicu  
s]//2.7e-79:393:96//Hs.19121:AI125280  
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:  
95//Hs.30464:AF091433  
R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:AI361807  
R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507  
R-PLACE1006205//EST//1.7e-89:448:96//Hs.116665:AA669114  
R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.9  
0:304:58//Hs.94986:U77664  
R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555  
R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472



R-nnnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142

R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.m usculus]//1.3e-104:532:95//Hs.41151:AI301961

R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548

R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839

R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132

R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265

R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503

R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900

R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168

R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044

R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284

R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053

R-PLACE1006382

R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748

R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881

R-PLACE1006414//Homo sapiens LIM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258

R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629

R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139

R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961

R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297

R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418

R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722

R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374  
R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:  
63//Hs.48824:D87717  
R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723  
R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368  
R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532  
R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214  
R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443  
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eI  
F3, p35 subunit mRNA, complete cds//9.3e-118:590:95//Hs.155377:U97670  
R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322  
R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615  
R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:  
78//Hs.101359:AB002384  
R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522  
R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627  
R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736  
R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214  
R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98/  
/Hs.12472:AF038172  
R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861  
R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//  
Hs.7252:AF070622  
R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658  
R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234  
R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515  
R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335  
R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989  
R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847

R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159  
R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO  
MOLOG [Homo sapiens]//1.0e-87:481:92//Hs.141263:H64113  
R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933  
R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA828359  
R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008  
R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536  
R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131  
R-nnnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348  
R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089  
R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13  
168  
R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514  
R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078  
R-nnnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:  
63//Hs.36927:D86956  
R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X5252  
0  
R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//  
9.0e-29:324:68//Hs.154257:AI275982  
R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636  
R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257  
R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366  
R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971  
R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6  
e-83:584:82//Hs.23094:M19503  
R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575  
R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027  
R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202

R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646  
 R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417  
 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948  
 R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794  
 R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765  
 R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998  
 R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619  
 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495  
 R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450  
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H.sapiens] /  
 /3.7e-73:357:98//Hs.18272:N78499  
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//H  
 s.121556:Y15909  
 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:AI275071  
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419  
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812  
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:7  
 4//Hs.154326:D42087  
 R-PLACE1007301  
 R-PLACE1007317  
 R-PLACE1007342  
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mR  
 NA, complete cds//1.2e-66:367:91//Hs.76596:AF096870  
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens] //2.2e-98:488:96//Hs.24359:AA699594  
 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614  
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945  
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877

R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771

R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens] //3.8e-115:579:95//Hs.72165:AI243857

R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171

R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514

R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230

R-PLACE1007478

R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975

R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker type s), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533

R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072

R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens] //1.5e-41:261:89//Hs.9029:W57657

R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377

R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087

R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612

R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404

R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840

R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179

R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176

R-PLACE1007632

R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106

R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946

R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNI  
NG ENTRY !!!! [H.sapiens]//9.0e-37:190:97//Hs.23437:AA707331

R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944

R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C  
HAIN 5 [Ascaris suum]//3.4e-61:384:89//Hs.92918:AA133274

R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces ce  
revisiae]//1.8e-84:501:88//Hs.91251:U66685

R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds  
//0.43:307:59//Hs.54481:D86407

R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/  
/5.7e-75:374:96//Hs.4812:AF061243

R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.eleg  
ans]//3.1e-39:253:88//Hs.108797:AA476815

R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619

R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.  
7e-94:556:89//Hs.153121:AB014585

R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322

R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778

R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903

R-PLACE1007791//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTE  
IN A [Bacillus subtilis]//8.6e-27:143:98//Hs.144194:AA706337

R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9  
e-45:428:76//Hs.23094:M19503

R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044

R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050

R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839

R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503

R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:AB018309

R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178

R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832

R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.92381:AB007956

R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510

R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966

R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.5671:AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:465:93//Hs.78106:AF079529

R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900

R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]//3.8e-97:493:95//Hs.6141:U69564

R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835

R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612

R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]//2.0e-115:575:95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935

R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269

R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469

R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334

R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617  
R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511  
R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381  
R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266  
R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267  
R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6  
e-104:551:93//Hs.10801:AB011102  
R-PLACE1008209//ESTs//1.2e-72:366:96//Hs.92308:AI052701  
R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871  
R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990  
R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808  
R-nnnnnnnnnnnnn  
R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705  
R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852  
R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.5  
3:206:62//Hs.79070:K02276  
R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.  
sapiens]//8.6e-79:297:91//Hs.146477:AI128445  
R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656  
R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1  
e-99:556:90//Hs.5734:AB014579  
R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052  
R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009  
R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
G ENTRY !!!! [H.sapiens]//2.0e-41:448:72//Hs.139007:H74314  
R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169  
:AA156242  
R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT



RY !!!! [H:sapiens]//1.2e-81:536:87//Hs.7570:W31010  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for pl15, complete cds//5.1e-103:521:9  
5//Hs.7763:D86326  
R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440  
R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778  
R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757  
R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562  
R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928  
R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761  
R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387  
R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636  
R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180  
R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816  
R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560  
R-PLACE1008532  
R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850  
R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223  
R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064  
R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens] /  
/8.6e-67:483:82//Hs.140416:AA778649  
R-nnnnnnnnnnnnn  
R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454  
R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972  
R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512  
R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612  
R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:  
79//Hs.153014:AB002353  
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, compl  
ete cds//7.9e-90:434:97//Hs.147967:AF044333

R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.  
51048:X68830

R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducibl  
e), polypeptide 2//1.7e-51:316:76//Hs.1361:M55053

R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600

R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !  
!!! [H.sapiens] //2.3e-40:281:83//Hs.142209:AA873303

R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408

R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313

R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930

R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217

R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 m  
RNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905

R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm1  
0e3 [C.elegans] //4.2e-92:490:93//Hs.110454:H11810

R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428

R-nnnnnnnnnnnnn

R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502

R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878

R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893

R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6  
e-56:344:89//Hs.62318:AB018308

R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018

R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653

R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSP  
ORTER 2 [Mus musculus] //1.3e-19:488:63//Hs.15780:U66680

R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573

R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419

R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.3

4780:AJ003112

R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520

R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195

R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139

R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008

R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R1  
OE12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9  
663:AA527142

R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448

R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:16  
1:63//Hs.77608:AL021546

R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.  
037:63:84//Hs.39943:AA203136

R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549

R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983

R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapien  
s]//6.5e-97:501:94//Hs.11123:AA703945

R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747

R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.  
norvegicus]//2.5e-36:163:82//Hs.93332:AA811920

R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005

R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322

R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948

R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707

R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717

R-PLACE1009186//ESTs, Weakly similar to No definition line found [C.eleg  
ans]//1.5e-109:572:94//Hs.54943:Z78396

R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701

R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X

98248

R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680

R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018

R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423

R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279

R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503

R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397

R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782

R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260

R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883

R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186

R-nnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798

R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255

R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632

R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269

R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872

R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427

R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:AC004531

R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925

R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596

R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698

R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131

R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apa f-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263

R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326

R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHA  
IN PRECURSORS [H.sapiens] //0.0012:56:91//Hs.12151:AA001818

R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.  
0e-42:547:70//Hs.69157:AB014535

R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735

R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482

R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680

R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338

R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858

R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701

R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.  
3e-109:589:92//Hs.21862:AB011159

R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens] /  
/9.9e-62:483:79//Hs.140416:AA778649

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:31  
0:97//Hs.109590:AF062534

R-PLACE1009708//ESTs//3.0e-94:471:96//Hs.40091:N48582

R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae] //4.2  
e-98:529:92//Hs.3945:AA004210

R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.  
musculus] //6.8e-85:489:89//Hs.26194:AA033989

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:59  
8:95//Hs.154320:AF046024

R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989

R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25  
-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3,  
EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein  
Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part o

f a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-113:549:97//Hs.16411:AL030996

R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868

R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748

R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328

R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031

R-nnnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:AI219740

R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563

R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276

R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI304317

R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543

R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074

R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540

R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347

R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219

R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736

R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204

R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//7.6e-104:546:94//Hs.8215:AA521150

R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905

R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.11183:AF065482

R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375

R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424

R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615  
R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.no  
rvegicus] //2.8e-104:565:92//Hs.11469:U69567  
R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015  
R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103  
R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens] //1.6e-  
107:575:93//Hs.48301:AA122270  
R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130  
R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359  
R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897  
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313  
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466  
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037  
R-PLACE1010231  
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478  
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545  
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535  
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788  
R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081  
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568  
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs  
.155464:AF088219  
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING  
ENTRY !!!! [H.sapiens] //9.9e-32:190:77//Hs.152369:AA504818  
R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327  
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594  
R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, p  
artial//4.9e-35:166:86//Hs.53531:AJ224162  
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152

R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:AF039081

R-PLACE1010492

R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031

R-nnnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455

R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306

R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033

R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116

R-PLACE1010599

R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418

R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895

R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475

R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:391:95//Hs.163495:W57637

R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805

R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719

R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102

R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:91//Hs.22383:R51067

R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659

R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973

R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mR



NA, partial cds//1.2e-56:300:95//Hs.50758:AF092564  
R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.  
.158122:AJ001189  
R-PLACE1010743  
R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48  
-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250  
R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024  
R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acantham  
oeba castellanii]//7.6e-111:575:94//Hs.10260:AI126627  
R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558  
R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203  
R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896  
R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472  
R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048  
R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]  
//1.4e-71:326:92//Hs.3385:N25917  
R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090  
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3  
e-101:501:96//Hs.118087:AB011182  
R-PLACE1010891  
R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983  
R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:  
U46023  
R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpi  
n)//0.25:190:61//Hs.75716:Y00630  
R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093  
R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479  
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3  
e-66:402:89//Hs.74750:AB011126

R-nnnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//  
 8.9e-82:441:93//Hs.66392:AF064244  
 R-PLACE1010944  
 R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519  
 R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs  
 .155464:AF088219  
 R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosoph  
 ila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437  
 R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580  
 R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846  
 R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867  
 R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4  
 e-102:563:91//Hs.41143:AB011153  
 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135  
 R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs  
 .155464:AF088219  
 R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537  
 R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
 RY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094  
 R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478  
 R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587  
 R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease vi  
 rus]//3.0e-105:552:93//Hs.31257:AA875998  
 R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795  
 R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:5  
 34:91//Hs.28719:AB015333  
 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673  
 R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !

!!! [H.sapiens]//3.4e-85:442:95//Hs.136910:AA810782  
R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438  
R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671  
R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299  
R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693  
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602  
R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772  
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913  
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849  
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807  
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572  
:U79291  
R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578  
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTE  
IN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337  
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376  
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194  
R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337  
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8  
e-114:600:94//Hs.10801:AB011102  
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7  
e-32:310:76//Hs.138488:AB014607  
R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887  
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.  
6e-104:515:96//Hs.111138:AB018255  
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278  
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.2  
8197:AF035294  
R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576

R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421  
 R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985  
 R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs  
 .8597:L11672  
 R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61  
 //Hs.78344:AF001548  
 R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067  
 R-PLACE1011641//ESTs//2.5e-71:338:100//Hs.153085:AA993965  
 R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900  
 R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//  
 Hs.78019:AF070535  
 R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036  
 R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filam  
 ent-associated protein)//0.50:178:62//Hs.31638:X64838  
 R-PLACE1011675  
 R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025  
 R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5  
 e-57:410:83//Hs.23094:M19503  
 R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392  
 R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426  
 R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative product  
 s} //7.3e-40:361:77//Hs.53217:Z48051  
 R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//  
 3.0e-60:319:76//Hs.103948:K00627  
 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080  
 R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF06  
 8179  
 R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563  
 R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:8

0//Hs.22271:D26067  
 R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648  
 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913  
 R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497  
 R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268  
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//  
 2.3e-99:546:92//Hs.3838:AF059617  
 R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969  
 R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOM  
 OLOG [H.sapiens] //2.6e-06:284:63//Hs.124102:AA701285  
 R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890  
 R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247  
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0  
 e-106:540:95//Hs.88756:AB018256  
 R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069  
 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//  
 4.8e-105:524:95//Hs.21811:AF091080  
 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211  
 R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504  
 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868  
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mR  
 NA//1.6e-43:355:79//Hs.154069:U06452  
 R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013  
 R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-4  
 5:514:72//Hs.96247:X95073  
 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated mo  
 lecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622  
 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.  
2e-41:429:72//Hs.153468:AB011147

R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:8  
6//Hs.40100:AB002390

R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6  
.2e-111:550:95//Hs.9443:AF027219

R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF06  
8179

R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236

R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941

R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,  
partial cds//0.00043:127:71//Hs.42400:AF022789

R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662

R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988

R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558

R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.  
7e-44:302:85//Hs.118401:AB011134

R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357

R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs  
.155464:AF088219

R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778

R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292

R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:9  
0//Hs.22271:D26067

R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378

R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191

R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717

R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.807  
06:M81600

R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363

R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens] //1.9e-87:422:98//Hs.9740:AI004779

R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOSOLIC [Homo sapiens] //4.8e-68:380:92//Hs.107365:AA720664

R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055

R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380

R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058

R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789

R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618

R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848

R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081

R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731

R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277

R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781

R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189

R-PLACE2000399

R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOSOLIC [Saccharomyces cerevisiae] //4.2e-109:540:96//Hs.6762:AA088424

R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941

R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans] //1.6e-97:436:95//Hs.24647:W19739

R-PLACE2000425//Homo sapiens DEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333

R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEE  
SI42F [C.elegans] //3.0e-113:543:97//Hs.16933:AA976002

R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523

R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986

R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887

R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:7  
4//Hs.40100:AB002390

R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714

R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638

R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228

R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642

R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838

R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.  
3e-64:350:86//Hs.153468:AB011147

R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763

R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979

R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.  
51048:X68830

R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727

R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739

R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792

R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369

R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142

R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815

R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223

R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen n  
ecrosis virus] //4.8e-36:262:88//Hs.31532:H18272

R-PLACE3000157

R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs



.155464:AF088219  
R-PLACE3000160  
R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798  
R-PLACE3000194  
R-PLACE3000197//ESTs//1.4e-38:197:98//Hs.146341:AI269930  
R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus  
scrofa]//0.018:261:61//Hs.131370:AA927516  
R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476  
R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084  
R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964  
R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717  
R-PLACE3000226//ESTs//1.3e-49:269:95//Hs.9059:AI359014  
R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878  
R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.7  
6313:U04811  
R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [  
Emericella nidulans]//7.5e-110:549:95//Hs.13692:AA632002  
R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:9  
4//Hs.87908:AB002307  
R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA,  
complete cds//2.3e-62:287:82//Hs.97203:U83171  
R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782  
R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phos  
phate 5-kinase (PIPK) mRNA, complete cds//4.0e-59:456:80//Hs.108966:U486  
96  
R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.  
51048:X68830  
R-PLACE3000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627  
R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo s

apiens]//5.8e-34:190:95//Hs.114531:N74103  
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.  
7e-32:239:84//Hs.15519:AB018315  
R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837  
R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688  
R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:2  
91:76//Hs.1721:X58377  
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380  
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683  
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888  
R-PLACE3000363  
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881  
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430  
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING  
ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534  
R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570  
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528  
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230  
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.  
142570:AF052160  
R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:31  
5:82//Hs.37181:D64108  
R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA,  
complete cds//4.4e-47:302:87//Hs.73614:U83460  
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077  
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs  
.155464:AF088219  
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs  
.32567:AF073519

R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461  
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899  
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980  
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227  
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352  
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240  
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031  
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292  
R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444  
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547  
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739  
R-PLACE4000100  
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931  
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] //3.8e-11:184:71//Hs.154278:N45985  
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969  
R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582  
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147  
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens] //6.7e-31:232:82//Hs.16493:T92186  
R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734  
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949  
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080

R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219

R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216

R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442

R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586

R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782

R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131

R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454

R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460

R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414

R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478

R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656

R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425

R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818

R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:AA778649

R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502

R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780

R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:AA643063

R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053

R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932

R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:AI334210

R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290

R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527

R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185

R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532

R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524

R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249

R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889

R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651

R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438

R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435

R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353

R-THYRO1000107//Interleukin 10//2.8e-43:292:84//Hs.2180:M57627

R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO MOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359

R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108

R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:AF087142

R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN G ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217

R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426

R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258

R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946

R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189

R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219

R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs

.155464:AF088219

R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6  
e-110:535:97//Hs.43445:AJ005698

R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.  
3e-115:559:97//Hs.79672:AB014552

R-THYR01000206//ESTs//3.1e-90:507:90//Hs.32456:W29063

R-THYR01000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT  
RY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349

R-THYR01000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.  
8e-69:524:82//Hs.141874:AB014588

R-THYR01000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYR01000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80/  
/Hs.80738:X52075

R-THYR01000270//ESTs//1.9e-99:531:94//Hs.17767:N62925

R-THYR01000279//EST//2.7e-54:266:99//Hs.149527:AI280674

R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:  
566:91//Hs.25846:AB016068

R-THYR01000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547

R-THYR01000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.8  
0731:M63175

R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4  
e-113:559:96//Hs.12002:AB018333

R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds  
//1.5e-48:317:87//Hs.7833:U29091

R-THYR01000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064

R-nnnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250

R-THYR01000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mR  
NA, complete cds//4.6e-69:294:84//Hs.151614:AF032456

R-THYR01000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081

R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429  
 R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601  
 R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638  
 R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans] //8.5e-40:239:90//Hs.84009:AI309761  
 R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426  
 R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:AB018280  
 R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333  
 R-THYRO1000501//ESTs//1.5e-46:287:89//Hs.125300:R62360  
 R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005  
 R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H.sapiens] //3.9e-57:286:96//Hs.105861:AI206965  
 R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511  
 R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193  
 R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485  
 R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:AF075587  
 R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247  
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223  
 R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens] //1.2e-96:483:96//Hs.21907:N24415  
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742  
 R-THYRO1000637  
 R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens] //4.9e-46:245:95//Hs.97398:AA398634  
 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840  
 R-nnnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384

R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866  
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063  
 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109  
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713  
 R-THYRO1000712  
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287  
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713  
 R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GAL  
 ACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.1  
 09672:W22624  
 R-THYRO1000777  
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932  
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897  
 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144  
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381  
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594  
 R-THYRO1000815//Human mRNA for KIAA0033. gene, partial cds//2.0e-56:307:8  
 7//Hs.22271:D26067  
 R-THYRO1000829  
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627  
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881  
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011  
 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA  
 dependent//2.8e-44:374:79//Hs.73821:M35663  
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871  
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234  
 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)  
 mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529  
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182



R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859  
R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761  
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440  
R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881  
R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524  
R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777  
R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131  
R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H. sapiens]//3.0e-57:341:91//Hs.44049:AA521489  
R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717  
R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070  
R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223  
R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497  
R-THYRO1001100  
R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834  
R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417  
R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399  
R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922  
R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853  
R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075  
R-THYRO1001177  
R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744  
R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151

R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932  
 R-THYRO1001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//  
 1.3e-48:349:83//Hs.139107:K00629  
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D  
 13640  
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561  
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269  
 R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230  
 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan sy  
 ndrome)//8.5e-05:326:60//Hs.82314:M31642  
 R-nnnnnnnnnnnnn//ESTs//0.16:422:59//Hs.23876:AA082935  
 R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:56  
 2:94//Hs.15032:AA774250  
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033  
 R-THYRO1001365  
 R-THYRO1001374  
 R-THYRO1001401//Human HsLIM15 mRNA for HsLim15, complete cds//2.5e-48:46  
 7:75//Hs.37181:D64108  
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627  
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733  
 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197  
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979  
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
 0508//9.1e-49:305:86//Hs.159187:AB007977  
 R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172  
 R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
 G ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082  
 R-THYRO1001480//Small inducible cytokine A5 (RANTES)//1.3e-40:331:79//Hs  
 .155464:AF088219

R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135

R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110

R-THYRO1001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094

R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936

R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594

R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413

R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958

R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741

R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247

R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288:67//Hs.85112:X57025

R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886

R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:dihydroxyacetonephosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190

R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874

R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282

R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//Hs.118633:AJ225089

R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957

R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726

R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691

R-THYRO1001721

R-nnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans] //1.7e-10:14  
7:77//Hs.158196:R53184

R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.  
116549:AL009172

R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323

R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474

R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224

R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788

R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA  
0487//5.7e-38:242:83//Hs.92381:AB007956

R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123

R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN  
G ENTRY !!!! [H.sapiens] //3.7e-41:362:79//Hs.139007:H74314

R-VESEN1000122

R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289

R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321

R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178

R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8  
e-51:330:89//Hs.153026:AB014540

R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629

R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792

R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.eleg  
ans] //2.4e-110:553:95//Hs.23159:AA113849

R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62/  
/Hs.79414:D79991

R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103

R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812

R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI246624

R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI092936  
R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs.84123:AB002363  
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826  
R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635  
R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210  
R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808  
R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//4.4e-66:339:97//Hs.8215:AA521150  
R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN G ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314  
R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018  
R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613  
R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758  
R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292  
R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-60:362:88//Hs.6381:AI188509  
R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320  
R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881  
R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.41723:U37426  
R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848  
R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:AI125280  
R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455  
R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:AF060503

R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE I  
N ATS1-TPD3 INTERGENIC REGION [*Saccharomyces cerevisiae*]//8.1e-27:140:10  
0//Hs.129049:H28818

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA  
, complete cds//8.7e-114:586:95//Hs.83023:AF093670

R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25  
B5.5 IN CHROMOSOME III [*C.elegans*]//9.8e-111:563:95//Hs.19845:AI005330

R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1  
701:L26405

R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:1  
00//Hs.84753:D87433

R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359

R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512

R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642

R-nnnnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405

R-Y79AA1000805

R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227

R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, comp  
lete cds//0.016:386:59//Hs.55836:U85647

R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079

R-Y79AA1000968

R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181

R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049

R-Y79AA1000985

R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851

R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067

R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407

R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325  
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.  
 8e-53:279:83//Hs.15731:AB011135  
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047  
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260  
 R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155  
 R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015  
 R-Y79AA1001167  
 R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884  
 R-Y79AA1001185  
 R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051  
 R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933  
 R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750  
 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674  
 R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892  
 R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271  
 R-Y79AA1001299//Human Inil mRNA, complete cds//9.6e-25:133:100//Hs.15562  
 6:U04847  
 R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI191149  
 R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084  
 R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143  
 R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819  
 R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859  
 R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891  
 R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2  
 -17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95//Hs.106616:AI027524  
 R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704

R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus] //6.2e-46:260:94//Hs.24884:AA176812

R-nnnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563

R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872

R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177

R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508

R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237

R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204

R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens] /7.2e-81:400:97//Hs.13323:AA897542

R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486

R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli] //2.5e-19:112:97//Hs.26252:AA643235

R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus] //9.7e-99:553:92//Hs.108896:R54040

R-nnnnnnnnnnnnn

R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783

R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490

R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12 . Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63//Hs.21864:AL031652

R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans] //9.4e-87:427:97//Hs.18645:AI023798

R-nnnnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:AA180809

R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.0 3c protein [H.sapiens] //8.1e-95:530:91//Hs.72444:W23217



R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582  
 R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs  
 .99931:L34355  
 R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:AI278630  
 R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094  
 R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652  
 R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404  
 R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275  
 R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.  
 69:93:73//Hs.15731:AB011135  
 R-Y79AA1002089//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:39  
 2:80//Hs.113283:AF018080  
 R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//H  
 s.78185:L38933  
 R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785  
 R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275  
 R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399  
 R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858  
 R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725  
 R-nnnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715  
 R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA syntheta-  
 se. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428  
 R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349  
 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING  
 PROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843  
 R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274  
 R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977  
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0  
 e-118:564:98//Hs.100729:AB014592

R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME  
[D.melanogaster]//9.0e-102:507:96//Hs.25895:AI341537  
R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4  
e-93:453:97//Hs.96731:AB014555  
R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288  
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1  
e-110:403:99//Hs.30898:AB014534  
R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985  
R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371  
R-Y79AA1002361  
R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908  
R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000  
R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753  
R-Y79AA1002431//EST//6.6e-23:128:98//Hs.128417:AA975026  
R-nnnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 6  
8 [Saccharomyces cerevisiae]//4.4e-62:390:88//Hs.143930:AI207821  
R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870  
R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788  
R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

【 0 8 2 9 】

相同性検索結果データ 6.

全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ。以下に示す検索結果には、比較配列の長さの単位にaaとbpが混在している。

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/Q61712  
C-HEMBA1000030  
C-HEMBA1000046  
C-HEMBA1000050

C-HEMBA1000076

C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553

C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5E-16//166aa//36%/P35584

C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662

C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555

C-HEMBA1000193

C-HEMBA1000227

C-HEMBA1000288

C-HEMBA1000302

C-HEMBA1000304

C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%/035594

C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%/AL049654

C-HEMBA1000387

C-HEMBA1000392

C-HEMBA1000460

C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%/Q04652

C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%/P22279

C-HEMBA1000501

C-HEMBA1000508

C-HEMBA1000520

C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%/P02826

C-HEMBA1000534

C-HEMBA1000555

C-HEMBA1000568

C-HEMBA1000588

C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179a  
a//61%//043295

C-HEMBA1000636

C-HEMBA1000682

C-HEMBA1000686

C-HEMBA1000719

C-HEMBA1000727

C-HEMBA1000752

C-HEMBA1000817

C-HEMBA1000851

C-HEMBA1000867

C-HEMBA1000869

C-HEMBA1000872

C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-X  
P ANTIGEN)//1.6E-30//127aa//40%//P43366

C-HEMBA1000918

C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN  
F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%//Q19124

C-HEMBA1000946

C-HEMBA1000968

C-HEMBA1000971

C-HEMBA1000975

C-HEMBA1001009

C-HEMBA1001022

C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHR  
OID) (FRAGMENT).//1.4E-12//131aa//38%//Q01485

C-HEMBA1001052  
C-HEMBA1001080  
C-HEMBA1001085  
C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%/P48059  
C-HEMBA1001109  
C-HEMBA1001122  
C-HEMBA1001133  
C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%/Q06730  
C-HEMBA1001140  
C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%/P51646  
C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%/AB020678  
C-HEMBA1001235  
C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%/AJ130733  
C-HEMBA1001281  
C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%/Q60401  
C-HEMBA1001303  
C-HEMBA1001310  
C-HEMBA1001326  
C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%/AF057358  
C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%/P17081  
C-HEMBA1001388  
C-HEMBA1001398

C-HEMBA1001405  
C-HEMBA1001407  
C-HEMBA1001413  
C-HEMBA1001415  
C-HEMBA1001446  
C-HEMBA1001450  
C-HEMBA1001455  
C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%/P18850  
C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37/  
/399aa//29%/P29166  
C-HEMBA1001533  
C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0  
//1662bp//99%/AB020657  
C-HEMBA1001581  
C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%/Q141  
41  
C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1  
.6E-10//155aa//28%/Q63679  
C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN  
).//4.6E-36//365aa//33%/P33450  
C-HEMBA1001702  
C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp5  
64G0422).//0//1845bp//99%/AL050386  
C-HEMBA1001731  
C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%/P53009  
C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%/P11  
675  
C-HEMBA1001815

C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52  
%/Q99676

C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%/Q  
07230

C-HEMBA1001864

C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%/P20659

C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (M  
E2GLYDH).//9.3E-36//395aa//26%/Q63342

C-HEMBA1001987

C-HEMBA1002018

C-HEMBA1002049

C-HEMBA1002084

C-HEMBA1002125

C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-5  
1//180aa//56%/P79293

C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E  
-13//190aa//36%/P43694

C-HEMBA1002191

C-HEMBA1002199

C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E  
-17//267aa//29%/P18161

C-HEMBA1002237

C-HEMBA1002265

C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//  
90%/AF125537

C-HEMBA1002349

C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mR  
NA, complete cds.//0//1847bp//99%/AF092563

C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%/P22793

C-HEMBA1002430

C-HEMBA1002439

C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//  
109aa//55%//Q00994

C-HEMBA1002460

C-HEMBA1002462

C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P9817  
5

C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.  
1E-12//285aa//31%//P17437

C-HEMBA1002477

C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa  
//36%//P48732

C-HEMBA1002515

C-HEMBA1002542

C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete  
cds.//6.8E-305//951bp//99%//AF075587

C-HEMBA1002583

C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.  
4E-253//1149bp//99%//AB011169

C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0  
//1539bp//99%//AB018351

C-HEMBA1002688

C-HEMBA1002696

C-HEMBA1002750

C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)  
.//1E-80//882bp//61%//AJ000414

C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0/  
/1532bp//99%//AB020636



C-HEMBA1002777

C-HEMBA1002794

C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cd  
s.//8.2e-314//1437bp//99%//AF071185

C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2E-304//1383bp//99%//A  
J132819

C-HEMBA1002850

C-HEMBA1002863

C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//  
1.5E-44//188aa//52%//Q09297

C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0/  
/1483bp//100%//AB011148

C-HEMBA1002937

C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./  
/2E-34//300aa//34%//P16157

C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0/  
/1752bp//99%//AB020710

C-HEMBA1002954

C-HEMBA1002971

C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1  
.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646

C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa/  
/24%//Q02224

C-HEMBA1003033

C-HEMBA1003035

C-HEMBA1003041

C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR  
(EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//075439

C-HEMBA1003067

C-HEMBA1003096

C-HEMBA1003117

C-HEMBA1003129

C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP  
-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)  
./8.5E-51//221aa//33%/P41940

C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EUROIMAG  
E 381801./0//1583bp//99%/AL079278

C-HEMBA1003175

C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METH  
YLTRANSFERASE (EC 2.1.1.61)./5.9E-74//134aa//53%/P44551

C-HEMBA1003199

C-HEMBA1003222

C-HEMBA1003235//TROPOMYOSIN./0.0000023//109aa//33%/Q02088

C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-)./7.2E-41//245aa//42%/  
/Q06548

C-HEMBA1003257

C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR./6E-11//239aa//32%/P3250  
6

C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV,  
complete cds./5.4E-229//1043bp//99%/AB024436

C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds./0  
//791bp//99%/AB011109

C-HEMBA1003322

C-HEMBA1003327

C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN)./0.00000002//248  
aa//23%/Q02224

C-HEMBA1003370

C-HEMBA1003380

C-HEMBA1003395

C-HEMBA1003402

C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0  
//1732bp//98%//AB020712

C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp58  
6C021).//1.6e-312//1414bp//99%//AL050287

C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%//P37709

C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%  
//AB013139

C-HEMBA1003447

C-HEMBA1003461

C-HEMBA1003463

C-HEMBA1003528

C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189  
//360aa//96%//P50480

C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//  
P53384

C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-  
2 SUBUNIT (G GAMMA-I).//1.2E-31//71aa//100%//P16874

C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//7.9E-49//279aa//32%//P19474

C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74  
%//Q13330

C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039

C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//  
4.4E-10//118aa//35%//P19682

C-HEMBA1003615

C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//50  
1bp//97%//AB015344

C-HEMBA1003621

C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q1  
3207

C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973

C-HEMBA1003711

C-HEMBA1003807

C-HEMBA1003864

C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAG  
MENT).//3.8E-16//89aa//46%//P16372

C-HEMBA1003959

C-HEMBA1003989

C-HEMBA1004074

C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complet  
e cds.//8.5E-221//1188bp//78%//AF091234

C-HEMBA1004146

C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0/  
/1893bp//98%//AB023145

C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, compl  
ete cds.//0//1892bp//99%//U50748

C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete  
cds.//5.7E-217//1217bp//88%//AF095927

C-HEMBA1004246

C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, co  
mplete cds.//4.8E-257//738bp//99%//AF092094

C-HEMBA1004289

C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512  
bp//96%//AF132955

C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1  
.2e-316//1445bp//99%//AF089841

C-HEMBA1004596

C-HEMBA1004693

C-HEMBA1004736

C-HEMBA1004753

C-HEMBA1004756//Human transporter protein (gl7) mRNA, complete cds.//9.1  
E-34//515bp//66%//U49082

C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds  
.//2.6E-246//1249bp//94%//L39060

C-HEMBA1004763

C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//  
58%//P08547

C-HEMBA1004771

C-HEMBA1004776

C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P508  
51

C-HEMBA1004806

C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E  
-154//317aa//94%//Q00004

C-HEMBA1004850

C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp5  
86M2022).//0//1443bp//100%//AL080114

C-HEMBA1004923

C-HEMBA1004929

C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27  
//65aa//100%//Q16401

C-HEMBA1004933

C-HEMBA1004954

C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR  
OTEIN) (NF-H).//0.00000096//286aa//23%//P12036

C-HEMBA1005475

C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%//P16372

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043

C-HEMBA1006377

C-HEMBA1006467

C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552

C-HEMBA1006530

C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.000000043//111aa//40%//Q01485

C-HEMBA1006795

C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258

C-HEMBA1006936

C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//AF078849

C-HEMBA1007342

C-HEMBB1000008

C-HEMBB1000018

C-HEMBB1000024

C-HEMBB1000025

C-HEMBB1000036

C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%//AF084928

C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%

//P11799

C-HEMBB1000103

C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521

C-HEMBB1000136

C-HEMBB1000215

C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI  
CASE EEED8.5.//2.7E-12//112aa//47%/Q09530

C-HEMBB1000244

C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN  
ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%/Q23256

C-HEMBB1000338

C-HEMBB1000339

C-HEMBB1000391

C-HEMBB1000438

C-HEMBB1000449

C-HEMBB1000589

C-HEMBB1000591

C-HEMBB1000623

C-HEMBB1000630

C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTO  
R 1).//4.1E-19//232aa//28%/P78970

C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//2  
73aa//31%/P27671

C-HEMBB1000671

C-HEMBB1000673

C-HEMBB1000705

C-HEMBB1000706

C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cd  
s.//6.2E-130//692bp//93%/U53475

C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676  
bp//96%//AF151847

C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kin  
ase MEKK2 mRNA, complete cds.//1.2E-126//613bp//97%//AF111105

C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERG  
ENIC REGION.//5.1E-54//232aa//43%//P39956

C-HEMBB1000807

C-HEMBB1000810

C-HEMBB1000848

C-HEMBB1000852

C-HEMBB1000870

C-HEMBB1000887

C-HEMBB1000908

C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//59  
5bp//76%//AF120102

C-HEMBB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA  
, complete cds.//0//2292bp//99%//AF116910

C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E  
-120//580bp//67%//AF099974

C-HEMBB1000975

C-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PRO  
TEIN).//8.6E-18//178aa//30%//P28575

C-HEMBB1000991

C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E  
-73//230aa//45%//P51523

C-HEMBB1001014

C-HEMBB1001024

C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION  
-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087



C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.6E-52//331bp//80%//AF010144  
C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803  
C-HEMBB1001096  
C-HEMBB1001105  
C-HEMBB1001117  
C-HEMBB1001126  
C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435  
C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267  
C-HEMBB1001153  
C-HEMBB1001169  
C-HEMBB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357  
C-HEMBB1001182  
C-HEMBB1001199  
C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187  
C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF 4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897  
C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966  
C-HEMBB1001289  
C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081  
C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703  
C-HEMBB1001331  
C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98

175

C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA,  
nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//29  
2bp//99%//AF097441

C-HEMBB1001369

C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds./  
/0//1586bp//99%//AF100757

C-HEMBB1001387

C-MAMMA1002317

C-MAMMA1002319

C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926

C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190

C-NT2RM1000242

C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028

C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE  
D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P  
39942

C-NT2RM1000669

C-NT2RM1000781

C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798b  
p//99%//AF092138

C-NT2RM1001008

C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//9  
80bp//95%//AF085360

C-NT2RM1001074

C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239  
aa//27%//

C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.  
11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete

sequence.//0//1740bp//99%//AL031291

C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167

C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703

C-NT2RM2000032

C-NT2RM2000042

C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102

C-NT2RM2000093

C-NT2RM2000101

C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223

C-NT2RM2000192

C-NT2RM2000239

C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2e-314//1416bp//100%//AL080069

C-NT2RM2000259

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181aa//34%//P14918

C-NT2RM2000287

C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//AB020666

C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA

, partial cds.//0//1506bp//99%/U48251  
 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.7E-68//419aa//36%/P50849  
 C-NT2RM2000374  
 C-NT2RM2000395.  
 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.6E-54//344aa//33%/P32802  
 C-NT2RM2000407  
 C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%/Q08469  
 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//157aa//28%/P36113  
 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.000089//377aa//24%/P22211  
 C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.8E-13//166aa//34%/P41823  
 C-NT2RM2000502  
 C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%/AF061243  
 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%/P17437  
 C-NT2RM2000540  
 C-NT2RM2000567  
 C-NT2RM2000569  
 C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.7E-187//741aa//46%/P73505  
 C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%/D86987  
 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%/P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487

C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//AF179221

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%//Q08170

C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272

C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558

C-NT2RM2000639

C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576

C-NT2RM2000669

C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391

C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.8E-23//184aa//36%//Q15404

C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342

C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//P41877

C-NT2RM2000795

C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.5E-279//545aa//98%//P23514

C-NT2RM2000837

C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//AB015046

C-NT2RM2000952

C-NT2RM2000984

C-NT2RM2001004

C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//  
Q60809

C-NT2RM2001065

C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.  
//2.4E-15//266aa//26%//P46577

C-NT2RM2001131

C-NT2RM2001141

C-NT2RM2001152

C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp5  
86G1822).//2.1E-293//1335bp//99%//AL080109

C-NT2RM2001194

C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//3  
5%//P05143

C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//0.0  
0000015//95aa//35%//P48724

C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP  
10).//3.6E-10//177aa//32%//P97924

C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)  
(L-GLUTAMINE AMIDOHYDROLASE).//1.3E-180//328aa//99%//P13264

C-NT2RM2001243

C-NT2RM2001247

C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166  
//312aa//98%//P53995

C-NT2RM2001291

C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp56  
4I052).//0//1694bp//99%//AL080063

C-NT2RM2001312

C-NT2RM2001319  
C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584  
C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000002  
9//334aa//22%//Q00808  
C-NT2RM2001370  
C-NT2RM2001393  
C-NT2RM2001420  
C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp5  
86D0920).//0//1621bp//100%//AL050146  
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (  
CAT2).//7.4E-121//437aa//57%//P52569  
C-NT2RM2001504  
C-NT2RM2001524  
C-NT2RM2001544  
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.  
3.4.1).//6.9E-27//90aa//42%//P38660  
C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//4.3E-61//312aa//44%//P19474  
C-NT2RM2001582  
C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0  
//1000bp//100%//AB014610  
C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692  
C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0/  
/2390bp//99%//AB007931  
C-NT2RM2001930  
C-NT2RM2001935  
C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27  
//216aa//34%//P28320  
C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC RE

GION.//0.0000001//212aa//23%/P38250

C-NT2RM2001982

C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%/P37838

C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//28%/Q12730

C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%/Q09782

C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.000000029//83aa//44%/P40796

C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%/P46837

C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%/AB016789

C-NT2RM2002049

C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.0000099//338aa//24%/Q07878

C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%/Q61990

C-NT2RM2002091

C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840

C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435

C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%/P49695

C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805

C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp4



34E0335).//0//1683bp//99%//AL117402  
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2  
 .7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167  
 C-NT2RM4000061  
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742  
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101  
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//4.8E-13//  
 686aa//23%//P25386  
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439a  
 a//41%//P16381  
 C-NT2RM4000197  
 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0  
 //1926bp//100%//AB018255  
 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-11  
 0) mRNA, complete cds.//1.1E-27//633bp//64%//L20303  
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, comp  
 lete cds.//2.2E-276//1124bp//97%//M99438  
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1  
 L.//0//2030bp//99%//AJ132637  
 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%  
 //AF083246  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21/  
 /208aa//35%//Q24371  
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//  
 86%//AB025412  
 C-NT2RM4000395  
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//17  
 30bp//99%//AJ133769  
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I

./8E-20//393aa//24%/Q10297

C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifs) mRNA, complete  
cds.//0//2092bp//99%/AF097025

C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4  
AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//  
31%/P04280

C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955

C-NT2RM4000511

C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PR  
OTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884

C-NT2RM4000520

C-NT2RM4000585

C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box prote  
in FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%/AF186273

C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0/  
/1940bp//95%/AB014587

C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0  
//1652bp//99%/AB020657

C-NT2RP1000040

C-NT2RP1000063

C-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//0//1162b  
p//99%/X98834

C-NT2RP1000101

C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%/P93471

C-NT2RP1000112

C-NT2RP1000124

C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//  
60%/P51859

C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0

//1889bp//98%//AB023165

C-NT2RP1000170

C-NT2RP1000191

C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357

C-NT2RP1000243

C-NT2RP1000259

C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730

C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551

C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447

C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343

C-NT2RP1000357

C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187

C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159

C-NT2RP1000416

C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423

C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257

C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580

C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653

C-NT2RP1000481

C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0

//2728bp//99%//D87686

C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020

C-NT2RP1000574//HOMEODOMAIN PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367

C-NT2RP1000581

C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233

C-NT2RP1000688

C-NT2RP1000695

C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379

C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434

C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//035566

C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960

C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1. (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223

C-NT2RP1000846

C-NT2RP1000851

C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//035566

C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.6E-105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%  
//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete  
cds.//2.5E-236//966bp//99%//M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338

C-NT2RP1000980

C-NT2RP1000988

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mR  
NA, complete cds.//2.2E-78//1529bp//61%//L01790

C-NT2RP1001014

C-NT2RP1001395

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//  
67%//P91917

C-NT2RP1001424

C-NT2RP1001449

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family pro  
tein (putative).//1.2E-137//629bp//100%//AJ005257

C-NT2RP1001466

C-NT2RP1001475

C-NT2RP1001482

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1  
.6E-166//506aa//60%//P42803

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27)  
(MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//03  
5566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BE  
TA).//5.8E-121//271aa//89%//P47758

C-NT2RP1001616

C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40)  
).//9.8E-17//79aa//55%//034136

C-NT2RP2000007

C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER. PROTEIN HPF2).//2.4E  
-177//726aa//47%//P51523

C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)  
.//1.8E-22//184aa//34%//Q01730

C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol  
og (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749

C-NT2RP2000054

C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3  
.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%//P49446

C-NT2RP2000067

C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN  
).//3.4E-51//383aa//32%//P33450

C-NT2RP2000079

C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0/  
/2286bp//100%//AB018338

C-NT2RP2000091

C-NT2RP2000097

C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//22  
44bp//99%//AB018356

C-NT2RP2000120

C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117  
//541aa//42%//P41877

C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0/  
/2286bp//99%//AB023206

C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%/P35585

C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%/P41891

C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%/Q09329

C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%/AB023225

C-NT2RP2000173

C-NT2RP2000175

C-NT2RP2000195

C-NT2RP2000205

C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%/AB020699

C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%/P35568

C-NT2RP2000232

C-NT2RP2000233

C-NT2RP2000239

C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%/P56558

C-NT2RP2000270

C-NT2RP2000274

C-NT2RP2000283

C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//25%/Q10297

C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%/Q99676

C-NT2RP2000298

C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA  
, complete cds.//4.3E-279//1193bp//99%//U82381

C-NT2RP2000328

C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760

C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.  
//6.3E-115//674aa//46%//P17564

C-NT2RP2000369

C-NT2RP2000412

C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.  
3E-228//415aa//100%//P52597

C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,  
complete cds.//0//1757bp//99%//AF102265

C-NT2RP2000438

C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844

C-NT2RP2000503

C-NT2RP2000510

C-NT2RP2000516

C-NT2RP2000603

C-NT2RP2000617

C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0/  
/2482bp//99%//AB014514

C-NT2RP2000656

C-NT2RP2000658

C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E  
-27//349aa//32%//Q01577

C-NT2RP2000704

C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA



LIGASE)//2.7E-100//488aa//44%//032038  
C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623  
C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0/  
/3347bp//99%//AB020680  
C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.00  
0000056//179aa//29%//Q99104  
C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//  
0.00000011//96aa//29%//P13466  
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//  
28%//P26174  
C-NT2RP2000819  
C-NT2RP2000841  
C-NT2RP2000845  
C-NT2RP2000863  
C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//  
99%//060841  
C-NT2RP2000892  
C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%//P43244  
C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp56  
40043).//0//2487bp//99%//AL050390  
C-NT2RP2000938  
C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0  
//3458bp//99%//AB018298  
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//  
96%//AB024704  
C-NT2RP2000985  
C-NT2RP2001036  
C-NT2RP2001044  
C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0488.//0//2749bp//99%//AB007957

C-NT2RP2001065

C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5)  
(PNP/PMP OXIDASE).//5.8E-46//222aa//45%//Q20939

C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%//P50232

C-NT2RP2001094

C-NT2RP2001119

C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ  
132440

C-NT2RP2001218

C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHA  
IN) (NMMHC).//2.2E-10//366aa//28%//P14105

C-NT2RP2001381

C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp43  
4B174).//0//1495bp//100%//AL080146

C-NT2RP2001427

C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0/  
/1748bp//99%//AB018340

C-NT2RP2001675

C-NT2RP2001721

C-NT2RP2001907

C-NT2RP2001969

C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA  
, complete cds.//4.7E-177//1538bp//74%//AF062378

C-NT2RP2002046

C-NT2RP2002154

C-NT2RP2002208

C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%//P42568

C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16

521

C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//158bp//99%//AB015594

C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%//AF038958

C-NT2RP2002426

C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//AB005289

C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%//Q11073

C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%//P12815

C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%//P55345

C-NT2RP2002621

C-NT2RP2002672

C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//30%//O14345

C-NT2RP2002769

C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%//P29764

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392

C-NT2RP2002954

C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669

C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P1012

9

C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190

C-NT2RP2003108

C-NT2RP2003117

C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%//AF079765

C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%  
//Q04652

C-NT2RP2003177

C-NT2RP2003194

C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580  
bp//99%//AF151811

C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572

C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14/  
/332aa//32%//P26337

C-NT2RP2003367

C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//  
269aa//91%//P38378

C-NT2RP2003446

C-NT2RP2003533

C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1  
.1.-).//1.7E-17//148aa//34%//P74261

C-NT2RP2003596

C-NT2RP2003629

C-NT2RP2003687

C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
).//5.4E-29//85aa//72%//Q05481

C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (U

BIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669

C-NT2RP2003793

C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//009175

C-NT2RP2003986

C-NT2RP2004042

C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820

C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120

C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044

C-NT2RP2004463

C-NT2RP2004602

C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291

C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//33%//Q92355

C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490

C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN P RECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588

C-NT2RP2004802

C-NT2RP2004841

C-NT2RP2004936

C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%/P13692  
C-NT2RP2004999  
C-NT2RP2005000  
C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0  
//1694bp//99%/AB014515  
C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%/AJ  
011779  
C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%/P32447  
C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box  
protein).//0//2388bp//98%/X98743  
C-NT2RP2005140  
C-NT2RP2005147  
C-NT2RP2005159  
C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete  
cds.//0//2087bp//99%/AF097025  
C-NT2RP2005270  
C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cd  
s.//0//2122bp//99%/D89053  
C-NT2RP2005293  
C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0/  
/1515bp//99%/AB014576  
C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protei  
n MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%/AF072247  
C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%/Q13823  
C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI  
NG FACTOR SRP75).//1.2E-13//185aa//38%/Q08170  
C-NT2RP2005441  
C-NT2RP2005453  
C-NT2RP2005464

C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//  
P38127

C-NT2RP2005472

C-NT2RP2005495

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPH  
A ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55  
).//5.2E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825  
bp//99%//AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mR  
NA, complete cds.//0//3994bp//99%//AF092563

C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.4E-304//1  
687bp//85%//AF035526

C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0  
//2856bp//99%//AB007963

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGL  
YOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTAS  
E) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39  
366

C-NT2RP2005555

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphat  
e phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//145  
5bp//98%//AF062085

C-NT2RP2005622

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).  
//1E-11//128aa//36%//P47623

C-NT2RP2005637

C-NT2RP2005640

C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%/P56101

C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%/AJ010973

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%/AF089814

C-NT2RP2005683

C-NT2RP2005690

C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%/AB018342

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.000000003//169aa//28%/P38074

C-NT2RP2005748

C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%/AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%/AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%/P47943

C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%/X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%/AF151351

C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%/Q02038

C-NT2RP2005781

C-NT2RP2005804

C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%/P34223



C-NT2RP2005853  
C-NT2RP2005868  
C-NT2RP2005886  
C-NT2RP2005890  
C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0  
//1977bp//99%//AB023188  
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//  
155aa//34%//P48837  
C-NT2RP2006038  
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI  
NG FACTOR SRP75).//1.5E-13//185aa//38%//Q08170  
C-NT2RP2006052  
C-NT2RP2006069  
C-NT2RP2006071  
C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp56  
4B102).//0//1759bp//99%//AL049970  
C-NT2RP2006106  
C-NT2RP2006141  
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.  
3E-189//899bp//97%//AB014554  
C-NT2RP2006196  
C-NT2RP2006200  
C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%  
//X96484  
C-NT2RP2006237  
C-NT2RP2006238  
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN  
LC1].//2E-59//388aa//32%//P46821  
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274

//1236bp//99%//AF035262

C-NT2RP2006333

C-NT2RP2006365

C-NT2RP2006393

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//0.00000034//50aa//50%//Q61658

C-NT2RP2006456

C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266

C-NT2RP2006467

C-NT2RP2006472

C-NT2RP2006565//Sus scrofa mRNA for SCAMP1 protein.//0//1276bp//84%//Y15710

C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPI1G1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461

C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543

C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708

C-NT2RP3000072

C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164

C-NT2RP3000220

C-NT2RP3000251

C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334

C-NT2RP3000312

C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Spl.//0//1544bp//100%//AJ242978

C-NT2RP3000333

C-NT2RP3000348

C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.000000028//185aa  
//31%//025074

C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760

C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219

C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293

C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.7E-139//679aa//41%//043143

C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185

C-NT2RP3000484

C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160

C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//P15151

C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283

C-NT2RP3000599

C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523

C-NT2RP3000644

C-NT2RP3000661

C-NT2RP3000665

C-NT2RP3000690

C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650

C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//

Q61982

C-NT2RP3000836

C-NT2RP3000841

C-NT2RP3000850

C-NT2RP3000852

C-NT2RP3000859

C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%//U53445

C-NT2RP3000869

C-NT2RP3000901

C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds.//0//3199bp//99%//AF064257

C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%//AF015264

C-NT2RP3000980

C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159

C-NT2RP3001004

C-NT2RP3001081

C-NT2RP3001084

C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.7E-94//787bp//66%//AF087433

C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201

C-NT2RP3001109

C-NT2RP3001116

C-NT2RP3001119

C-NT2RP3001133

C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305

C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ  
006266

C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REG  
ION.//1.7E-10//196aa//27%//P53154

C-NT2RP3001214

C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0  
000023//137aa//33%//P35663

C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.  
11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

C-NT2RP3001236

C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CO  
NTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%//P14873

C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0  
//2497bp//99%//AB020718

C-NT2RP3001307

C-NT2RP3001325

C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase ancho  
ring protein 95, complete cds.//0//1213bp//99%//AB025905

C-NT2RP3001392

C-NT2RP3001396

C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%//P4  
9711

C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009

C-NT2RP3001420

C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%//033529

C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//  
009053

C-NT2RP3001457

C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%//

P11632

C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1  
475bp//99%//U13395

C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (T  
RC8) mRNA, complete cds.//0//2295bp//99%//AF064801

C-NT2RP3001529//SP00B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%  
//P20964

C-NT2RP3001621

C-NT2RP3001629

C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q926  
09

C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468

C-NT2RP3001676

C-NT2RP3001679

C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27  
%//P24733

C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%  
//Q04652

C-NT2RP3001896

C-NT2RP3001915

C-NT2RP3001929

C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742

C-NT2RP3004466

C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E  
-113//466aa//42%//P34110

C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0/  
/1520bp//99%//AB014532

C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0/  
/974bp//95%//AB011126

C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHR  
OID).//0.000000038//150aa//28%//Q01484

C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA  
A, complete cds.//0//1770bp//99%//AF026445

C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0  
//1639bp//99%//AB007946

C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ  
006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, comp  
lete cds.//0//3972bp//98%//AF093097

C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEI  
N).//1.7E-72//254aa//45%//P54352

C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P355  
26

C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.9E-51//335aa//37%/  
/Q64375

C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0  
//3013bp//99%//AB020657

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99  
%//AB011538

C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568

C-NT2RP4000129

C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating  
protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150

C-NT2RP4000151

C-NT2RP4000159

C-NT2RP4000185

C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0/  
/4149bp//99%//AB014600

C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15  
//104aa//40%//P15287

C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP  
).//0//1932bp//99%//AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//2  
08aa//76%//Q03173

C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa/  
/43%//O23968

C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.  
//3.5E-297//1024aa//55%//P87115

C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)  
(ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631

C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).  
//0.0000003//101aa//32%//P26372

C-NT2RP4000355

C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0  
//4074bp//99%//AB018281

C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP)  
mRNA, complete cds.//0//4782bp//99%//AF044195

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).  
//2.6E-77//262aa//54%//O75570

C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.  
n.//0//2412bp//99%//AJ238243

C-NT2RP4000381

C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738

C-NT2RP4000415



C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%/P45701

C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%/AL050078

C-NT2RP4000449

C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%/P09309

C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%/P50101

C-NT2RP4000480

C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%/Q09475

C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%/P40484

C-NT2RP4000500

C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%/P45818

C-NT2RP4000524

C-NT2RP4000541

C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%/P40319

C-NT2RP4000560

C-NT2RP4000588

C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%/AF067730

C-NT2RP4000638

C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%/P09309

C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.  
1E-32//350aa//30%/P39625

C-NT2RP4000704

C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1  
.1E-13//295aa//27%/Q11073

C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78  
%/P10267

C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0/  
/3392bp//95%/AB023148

C-NT2RP4000737

C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0  
//3574bp//99%/AB023229

C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC RE  
GION.//0.000000032//67aa//31%/P53915

C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0  
//1927bp//99%/AB007939

C-NT2RP4000833

C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-9  
4//810bp//65%/Y18265

C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//2  
71aa//28%/Q00808

C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.7E-82//3  
24aa//48%/009175

C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//  
55%/P16415

C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%/03568

2

C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96/

/513aa//42%/P22314

C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROT  
EIN).//2.6E-26//227aa//36%/Q06828

C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15  
) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEAS  
E DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%/Q61068

C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%/Y16  
521

C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014/  
/185aa//25%/Q58900

C-NT2RP4000955

C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.  
3.4.1).//1.4E-26//90aa//42%/P38660

C-NT2RP4000975

C-NT2RP4000979

C-NT2RP4000984

C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%/P34579

C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7  
.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%/P70700

C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%/P39968

C-NT2RP4001006

C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0  
//2482bp//99%/AB023181

C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T  
RNA LIGASE)//1.5E-92//443aa//44%/Q09996

C-NT2RP4001057

C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%/  
/Q64375

C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-

ATPASE).//1.3E-123//563aa//46%/P13586  
 C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99  
 %//AB023967  
 C-NT2RP4001086  
 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSR  
 NA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%/P5  
 1400  
 C-NT2RP4001100  
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115  
 //224aa//100%/P38378  
 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%/O15736  
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%/Q07283  
 C-NT2RP4001138  
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SD  
 AP).//0.00000021//93aa//33%/P44514  
 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%/P33750  
 C-NT2RP4001149  
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM)  
 (BRAVO).//3.4E-29//385aa//29%/P35331  
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSO  
 R (CTPT).//4.7E-29//227aa//35%/P52178  
 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, com  
 plete cds.//4.4E-104//1460bp//65%/U95760  
 C-NT2RP4001207  
 C-NT2RP4001210  
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.  
 3.4.1).//6.2E-27//90aa//42%/P38660  
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43  
 %//Q04652

C-NT2RP4001235

C-NT2RP4001256

C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0/  
/2876bp//99%//AB020682

C-NT2RP4001274//Human transporter protein (gl7) mRNA, complete cds.//4.4  
E-58//1196bp//61%//U49082

C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%//Q07283

C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTE  
IN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/  
/P24391

C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5  
.//8.5E-213//1129bp//92%//AJ001119

C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp/  
/99%//AJ007014

C-NT2RP4001343

C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL)  
, complete cds.//2.7e-310//1400bp//100%//AB017494

C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain ho  
molog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%//U53445

C-NT2RP4001353

C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PRO  
TEIN).//1.6E-19//222aa//30%//Q08180

C-NT2RP4001373

C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112  
) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%//P18160

C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//  
2E-53//436aa//30%//Q10085

C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0  
//2716bp//99%//AB023140

C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q141  
41

C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54  
%//Q99676

C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, compl  
ete cds.//2.7E-66//738bp//71%//AF129131

C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC  
1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218

C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//2  
9%//P39010

C-NT2RP4001502

C-NT2RP4001507

C-NT2RP4001524

C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENI  
C REGION.//5.7E-54//242aa//38%//P25656

C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation  
factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%//AF1529  
61

C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa  
//24%//P96902

C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//  
26%//Q02453

C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197

C-NT2RP4001571

C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds./  
/0//3046bp//99%//AF100756

C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%  
//AJ223830

C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA

LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505  
 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0/  
 /1897bp//99%/AB020676  
 C-NT2RP4001614  
 C-NT2RP4001634  
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//  
 234aa//32%/P40469  
 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-1  
 9//111aa//45%/P25323  
 C-NT2RP4001677  
 C-NT2RP4001679  
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
 SUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568  
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10/  
 /128aa//32%/Q10282  
 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (   
 EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332  
 C-NT2RP4001739  
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E  
 -236//665aa//58%/P51523  
 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO  
 /RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174  
 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0  
 //3144bp//99%/AB023232  
 C-NT2RP4001803  
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27)  
 (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/03  
 5566  
 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//5

4%/P55083

C-NT2RP4001828

C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.

//6.3E-99//555bp//73%//AF155595

C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%//P37709

C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%//AL050390

C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.000000014//345aa//25%//Q00808

C-NT2RP4001901

C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024

C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) .//1.5E-13//211aa//28%//Q43209

C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816

C-NT2RP4001953

C-NT2RP4001966

C-NT2RP4001975

C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652

C-NT2RP4002052

C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)///1E-137//679aa//40%//043143

C-NT2RP4002071



C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)  
).//3E-150//722aa//39%//Q05481  
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAIN  
S (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//3  
1%//P52655  
C-NT2RP4002298  
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//  
P38938  
C-NT2RP4002791  
C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F172 (from clone DKFZp43  
4F172).//0//2557bp//99%//AL080202  
C-NT2RP4002905  
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552  
C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//2  
80aa//27%//Q00808  
C-NT2RP5003492  
C-NT2RP5003500  
C-NT2RP5003506  
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3  
E-23//219aa//40%//P37116  
C-NT2RP5003524  
C-NT2RP5003534  
C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262  
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000  
042//102aa//32%//O14727  
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//  
1393bp//97%//AF058922  
C-OVARC1000035  
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (R

NASE LE).//0.00000032//60aa//45%/P80022  
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%/Q02874  
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1  
 ) (VCAF) (CFF).//8.4E-14//259aa//30%/P51610  
 C-OVARC1000113  
 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562  
 bp//99%/AF132955  
 C-OVARC1000148  
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 inter  
 acting with transcription factor Spl.//2.5E-95//461bp//98%/AJ242975  
 C-OVARC1000168  
 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, comple  
 te cds.//1.8E-32//511bp//65%/AF068332  
 C-OVARC1000212  
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INT  
 ERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-1  
 20//351aa//54%/Q16665  
 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLY  
 PEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III) (AMINO  
 PEPTIDASE YSCI).//5.4E-53//384aa//30%/P14904  
 C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%/P23249  
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%/P  
 29363  
 C-OVARC1000321  
 C-OVARC1000326  
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REG  
 ION.//5.9E-14//200aa//27%/P40004  
 C-OVARC1000347  
 C-OVARC1000384

C-OVARC1000411

C-OVARC1000420

C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205

C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//99%//AL080126

C-OVARC1000461

C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075

C-OVARC1000466

C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452

C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636

C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91%//AF051850

C-OVARC1000564

C-OVARC1000576

C-OVARC1000588

C-OVARC1000605

C-OVARC1000640

C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%//D43772

C-OVARC1000661

C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886

C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343

C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%  
 //AJ130978  
 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215/  
 /1027bp//98%//AF132946  
 C-OVARC1001162  
 C-OVARC1001243  
 C-OVARC1001296  
 C-OVARC1001360  
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involve  
 d in B-CLL.//6E-148//683bp//99%//AJ224819  
 C-OVARC1001425  
 C-PLACE1000005  
 C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538  
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONAS  
 E).//2.8E-29//134aa//43%//P52046  
 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5  
 .5e-312//1411bp//99%//AB020639  
 C-PLACE1000185  
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0  
 //1904bp//99%//AB023194  
 C-PLACE1000347  
 C-PLACE1000374  
 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0/  
 /2208bp//99%//AB020660  
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ2  
 24979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30/  
 /352aa//31%//P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//

72%/P23246

C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//0.0000028//134aa//29%/P53368

C-PLACE1000435

C-PLACE1000444

C-PLACE1000562

C-PLACE1000564

C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE- BINDING PROTEIN 1).//1.6E-270//437aa//86%/P32455

C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%/AB020657

C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%/AF044201

C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%/Q08891

C-PLACE1000716

C-PLACE1000748

C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.6E-250//1189bp//97%/AB028449

C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%/AB014548

C-PLACE1000798

C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.5E-49//181aa//54%/P32899

C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%/P39010

C-PLACE1000948

C-PLACE1000972

C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%/Q03070

C-PLACE1001000

C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//150  
0bp//99%//AF065485

C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%  
//Q04652

C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FING  
ER PROTEIN REQUIEM).//3E-33//138aa//42%//Q61103

C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8./  
/2.3E-61//132aa//46%//Q12929

C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete  
sequence.//0//2118bp//99%//AC005412

C-PLACE1001412

C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT S  
EQUENCE, in unordered pieces.//0//1440bp//99%//AL031660

C-PLACE1001503

C-PLACE1001570

C-PLACE1001610

C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (E  
C 3.1.2.14) (THIOESTERASE II).//4E-81//263aa//56%//P08635

C-PLACE1001729

C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA-HELICASE PL10.//3.5E-75//439a  
a//41%//P16381

C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63  
//427aa//35%//Q57290

C-PLACE1001810

C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta s  
ubunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953

C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524

C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0

//1196bp//99%//AF131737

C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//

1729bp//99%//AF099935

C-PLACE1001928

C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091

C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211

C-PLACE1002072

C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//0.00000053//188aa//29%//P49606

C-PLACE1002140

C-PLACE1002163

C-PLACE1002170

C-PLACE1002433

C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105

C-PLACE1002465

C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256

C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180

C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391

C-PLACE1002794

C-PLACE1002815

C-PLACE1002839

C-PLACE1002851

C-PLACE1002941

C-PLACE1002996

C-PLACE1003045

C-PLACE1003092

C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268

C-PLACE1003108

C-PLACE1003145

C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743

C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750

C-PLACE1003200

C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133

C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//P51522

C-PLACE1003334

C-PLACE1003342

C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715

C-PLACE1003369

C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200

C-PLACE1003611

C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824

C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%//Q08170

C-PLACE1003711

C-PLACE1003723

C-PLACE1003762



C-PLACE1003771  
 C-PLACE1003784  
 C-PLACE1003923  
 C-PLACE1003936  
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK G  
 AMMA-1 CHAIN).//2.4E-124//326aa//73%/P80385  
 C-PLACE1004104  
 C-PLACE1004114  
 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANS  
 DUCIN BETA CHAIN 4).//6.1E-181//340aa//96%/P29387  
 C-PLACE1004149  
 C-PLACE1004156  
 C-PLACE1004161  
 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%/AJ0  
 10071  
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%/Q6255  
 6  
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precu  
 sor, mRNA, complete cds.//0//1882bp//99%/AF069493  
 C-PLACE1004258  
 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36  
 //389aa//31%/O15393  
 C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, c  
 omplete cds.//0//1498bp//99%/AF084830  
 C-PLACE1004289  
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%/P33750  
 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767b  
 p//99%/Y11588  
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1

mRNA, complete cds.//0//2512bp//99%//AF100153  
C-PLACE1004376  
C-PLACE1004388  
C-PLACE1004405  
C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33  
%//Q63448  
C-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subuni  
t precursor, mRNA, nuclear gene encoding mitochondrial protein, complete  
cds.//0//985bp//99%//U49283  
C-PLACE1004451  
C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823  
C-PLACE1004473  
C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRN  
A, complete//1.3E-209//954bp//99%//AF026445  
C-PLACE1004516  
C-PLACE1004548  
C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD  
SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568  
C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%//Q13438  
C-PLACE1004645  
C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane re  
ceptor p63.//4.4E-42//985bp//59%//X66277  
C-PLACE1004664  
C-PLACE1004672  
C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)  
.//1.6E-95//191aa//96%//P12815  
C-PLACE1004691  
C-PLACE1004722  
C-PLACE1004736

C-PLACE1004740

C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LI  
GASE E3 COMPONENT) (N- RECOGNIN).//4.4E-35//578aa//27%/O60152

C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal  
VI, complete cds.//7.1E-224//790bp//98%/AB022918

C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAE  
RIN).//1.9E-32//259aa//32%/P30337

C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)  
(ADENYLYL CYCLASE).//4.7E-65//695aa//29%/Q01631

C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICI  
NG FACTOR SRP75).//5.9E-19//196aa//36%/Q08170

C-PLACE1004824

C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q08891

C-PLACE1004885

C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELI  
CASE SPAC10F6.02C.//9.3E-11//94aa//47%/042643

C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//  
4.9E-48//198aa//44%/P06151

C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1  
853bp//98%/AF099936

C-PLACE1004934

C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794

C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2  
E-14//205aa//26%/Q11073

C-PLACE1004982

C-PLACE1005026

C-PLACE1005027

C-PLACE1005046

C-PLACE1005077

C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209  
//1031bp//96%//L40401  
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%  
//Q04652  
C-PLACE1005111  
C-PLACE1005181  
C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636  
C-PLACE1005206  
C-PLACE1005232  
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E  
-27//349aa//32%//Q01577  
C-PLACE1005261  
C-PLACE1005266  
C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.  
2E-297//1341bp//100%//AB011182  
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%/  
/P53352  
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (  
AK3).//2E-111//226aa//92%//P08760  
C-PLACE1005308  
C-PLACE1005313  
C-PLACE1005327  
C-PLACE1005335  
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDO  
URIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL  
HYDROLYASE).//8.6E-09//194aa//27%//O33335  
C-PLACE1005374  
C-PLACE1005480  
C-PLACE1005481

C-PLACE1005494//Homo sapiens mRNA for transient receptor potential prote  
in TRP6.//0//1649bp//99%//AJ006276

C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.  
//5.6E-52//173aa//57%//Q09251

C-PLACE1005550

C-PLACE1005554

C-PLACE1005623

C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete  
cds.//0//2130bp//99%//AF083255

C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4  
.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350

C-PLACE1005730

C-PLACE1005755

C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (E  
C 3.1.2.14) (THIOESTERASE II).//2.5E-79//209aa//53%//P08635

C-PLACE1005803

C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds  
.//1.1E-217//994bp//99%//AF027156

C-PLACE1005851

C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120

C-PLACE1005923

C-PLACE1005925

C-PLACE1005934

C-PLACE1005936

C-PLACE1005951

C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//  
37%//P43636

C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLY  
PEPTIDASE)//5.4E-54//455aa//32%//P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAF II-90).//0.00000014//254aa//25%//P38129

C-PLACE1005990

C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876

C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906

C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//AF039023

C-PLACE1006139

C-PLACE1006159

C-PLACE1006167

C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706

C-PLACE1006195

C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747

C-PLACE1006225

C-PLACE1006236

C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//P28675

C-PLACE1006246

C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//1271bp//99%//AL080066

C-PLACE1006335

C-PLACE1006357

C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085

C-PLACE1006412

C-PLACE1006414

C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%/P49910

C-PLACE1006445

C-PLACE1006470

C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%/Q90595

C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%/Q00004

C-PLACE1006492

C-PLACE1006531

C-PLACE1006552

C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//2182bp//99%/AC007383

C-PLACE1006615

C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%/AB023145

C-PLACE1006673

C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%/AB015630

C-PLACE1006704

C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%/Q59263

C-PLACE1006782

C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%/P08547

C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%/P35123

C-PLACE1006883

C-PLACE1006901

C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181

C-PLACE1006932

C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//  
6.7E-48//278aa//41%//Q10000

C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P9799  
8.

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete  
cds.//0//1770bp//99%//AB023421

C-PLACE1006961

C-PLACE1006962

C-PLACE1006966

C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PR  
OTEIN 12) (DER12).//3.2E-35//180aa//33%//Q14542

C-PLACE1007021

C-PLACE1007105

C-PLACE1007178

C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDA  
SE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370a  
a//31%//P54304

C-PLACE1007238

C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-  
II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%//D50495

C-PLACE1007242

C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//  
Y15908

C-PLACE1007274



C-PLACE1007282

C-PLACE1007301

C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%//AF117649

C-PLACE1007342

C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870

C-PLACE1007367

C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715

C-PLACE1007386

C-PLACE1007402

C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487

C-PLACE1007450

C-PLACE1007452

C-PLACE1007460

C-PLACE1007484

C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734

C-PLACE1007507

C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%//P08728

C-PLACE1007524

C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164

C-PLACE1007544

C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III./  
/1E-49//361aa//36%//P34537

C-PLACE1007583

C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44  
%//Q99676

C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0  
//713bp//99%//AB023194

C-PLACE1007621

C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P  
32506

C-PLACE1007645

C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0  
//1952bp//99%//AB023194

C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGE  
N HOMOLOG).//8.7E-09//279aa//28%//Q26457

C-PLACE1007690

C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535

C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.  
//0//3431bp//99%//AF061243

C-PLACE1007725

C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231  
aa//42%//P10265

C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9  
.2E-294//1504bp//94%//AB014585

C-PLACE1007746

C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%/  
/AB019602

C-PLACE1007810

C-PLACE1007843

C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region  
, segment 3/13.//0//1751bp//99%//AP000010

C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0  
//3112bp//99%//AB018309

C-PLACE1007897

C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN  
II).//2.6E-14//370aa//25%//Q99323

C-PLACE1007954

C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, com  
plete cds.//0//2252bp//99%//AF084530

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)  
mRNA, partial cds.//0//2300bp//99%//AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.  
1E-36//202aa//48%//P52272

C-PLACE1007990

C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110)  
(SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622

C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//0//1833bp//99%//AC005628

C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107)  
(107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590

C-PLACE1008095

C-PLACE1008122

C-PLACE1008129

C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.  
//1.3E-24//395aa//31%//Q09531

C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709

C-PLACE1008209

C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).

//1.3E-283//671aa//77%/P53620

C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-)//2.3E-18//162aa//3

7%/P12689

C-PLACE1008280

C-PLACE1008309

C-PLACE1008329

C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0/

/1853bp//100%/AB014579

C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%/P05432

C-PLACE1008401

C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%/P41541

C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%/Q06527

C-PLACE1008457

C-PLACE1008465

C-PLACE1008488

C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1

-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine receptor)

//0//1980bp//99%/AL031778

/AL031778

C-PLACE1008531

C-PLACE1008532

C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%/P22620

C-PLACE1008568

C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155)

(155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%/P37199

C-PLACE1008621

C-PLACE1008626

C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp/  
/99%//AJ006591

C-PLACE1008629

C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333

C-PLACE1008693

C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406

C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//035345

C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1 A.//2.3E-269//1225bp//99%//AJ004974

C-PLACE1008813

C-PLACE1008854

C-PLACE1008867

C-PLACE1008887

C-PLACE1008902

C-PLACE1008925

C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623

C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112

C-PLACE1009045

C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582

C-PLACE1009090

C-PLACE1009091

C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2)

./1.9E-44//480aa//30%/P30432

C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%  
//P51814

C-PLACE1009110

C-PLACE1009111

C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PRO  
TEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%/Q05086

C-PLACE1009158

C-PLACE1009166

C-PLACE1009174

C-PLACE1009186

C-PLACE1009190

C-PLACE1009230

C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, c  
omplete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//  
75%/AF107295

C-PLACE1009328

C-PLACE1009335

C-PLACE1009338

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%/Q12  
067

C-PLACE1009375

C-PLACE1009388

C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.  
//0.000000047//165aa//33%/Q09820

C-PLACE1009434

C-PLACE1009443

C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-K  
INASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%/P42356

C-PLACE1009459

C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//  
550aa//93%//P54319

C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSO  
ME III.//3.9E-40//179aa//37%//P34580

C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF E  
XCHANGE FACTOR).//8.1E-99//228aa//75%//Q99418

C-PLACE1009542

C-PLACE1009571

C-PLACE1009581

C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//2  
91aa//40%//Q00808

C-PLACE1009607

C-PLACE1009621

C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P  
25159

C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.5E-  
285//538aa//99%//P55161

C-PLACE1009665

C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp  
//100%//AF062534

C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN  
C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876

C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200

C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120

C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, com  
plete cds.//4.3E-294//1329bp//100%//AB012190

C-PLACE1009794

C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0

//2685bp//99%//AB020712

C-PLACE1009886

C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENE  
C REGION.//1.9E-108//277aa//43%//P53145

C-PLACE1009971

C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6  
E-59//450aa//34%//P28175

C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp56  
40123).//0//1962bp//99%//AL080122

C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mR  
NA, complete cds.//5.2E-70//736bp//73%//U48288

C-PLACE1010023

C-PLACE1010031

C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1  
402bp//94%//X84692

C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./  
/0//2019bp//99%//AF065482

C-PLACE1010076

C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q626  
71

C-PLACE1010102

C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44  
%//Q04652

C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp5  
86M1418).//0//1974bp//99%//AL049385

C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX C  
OMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRAN  
SCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082

C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//43



1aa//23%//P35662

C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130

C-PLACE1010202

C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722

C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%//AL080122

C-PLACE1010293

C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%//P52178

C-PLACE1010324

C-PLACE1010329

C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.00000002//126aa//29%//P34024

C-PLACE1010364

C-PLACE1010383

C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%//AB020643

C-PLACE1010491

C-PLACE1010492

C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%//AB022718

C-PLACE1010529

C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//P25386

C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor

protein, complete cds.//0//1904bp//99%//AB017546  
C-PLACE1010616  
C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016/  
/120aa//28%//P02642  
C-PLACE1010629  
C-PLACE1010630  
C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01  
755  
C-PLACE1010714  
C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-  
C, complete cds.//4E-299//1091bp//99%//AB019987  
C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, par  
tial cds.//8.9E-91//668bp//82%//AF020267  
C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061  
C-PLACE1010786  
C-PLACE1010800  
C-PLACE1010811  
C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
) .//1.3E-143//407aa//58%//Q05481  
C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0/  
/1885bp//99%//AB011182  
C-PLACE1010900  
C-PLACE2000050  
C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH  
PROTEIN).//2.4E-191//828aa//48%//P21783  
C-PLACE4000590  
C-PLACE4000638  
C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17  
//201aa//34%//P49816

C-Y79AA1001647

【 0 8 3 0 】

相同性検索結果データ 7.

実施例 1 6 で選抜した 54 クロンの 5' 末端クローン配列に対する SwissProt 相同性検索結果データ

各データは、クローン配列名、トップヒットデータの Definition、P 値: 比較配列の長さ (base): 相同性 (%), トップヒットデータの Organism、トップヒットデータの Accession No. の順に // で区切って記載した。

なお、相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G). /  
/0.13//52//38//P25860

F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15)  
(UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64  
E) (DEUBIQUITINATING ENZYME 64E). //2.2e-28//104//59//Q24574

F-HEMBA1003854//VERPROLIN. //0.012//138//31//P37370

F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FR  
AGMENT). //0.93//39//33//Q37131

F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).  
//0.90//20//50//P38524

F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16). //7.6e-46//141//58//Q15  
973

F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT). //0.0033//32//46/  
/P70560

F-HEMBA1006092//VERPROLIN. //1.0//62//35//P37370

F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10). //0.30/  
/41//36//P12350

F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR. //0.089//21//52/  
/Q02593

F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY). //0.38

//156//30//P28697

F-HEMBB1000672

F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0//30//36//P16  
012

F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S  
1).//3.7e-54//241//47//P47853

F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3' REGION (ORF3).//0.  
59//48//39//Q51483

F-MAMMA1002094

F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.26//58  
//27//P06333

F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS  
E DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III  
) (FRAGMENT).//8.9e-20//83//48//P10895

F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT).//1.0//42//40//P19326

F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID  
LABILE CHAIN PRECURSOR (ALS).//6.0e-23//207//32//002833

F-NT2RM4001178//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.012//156//28//Q90267

F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0012//81//37//P  
13816

F-NT2RP2000198//CREB-BINDING PROTEIN.//0.29//98//37//Q92793

F-NT2RP2000551//PROTEIN Q300.//0.00017//23//60//Q02722

F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401.//1.0//41//29//Q57844

F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.27//13//61//Q016  
44

F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-).//0.089//99//29//Q990  
14

F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAG  
MENT).//4.0e-13//177//28//P16372

F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5' REGION.//0.37//12  
//75//P53820

F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)./  
/0.99//61//32//Q42616

F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2.//3.3e-10//90//35//Q06666

F-NT2RP2002843//CYTOCHROME B.//0.78//103//26//P48884

F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG.//0.40//28//46//  
P37209

F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1.//0.80//55//32//P81303

F-NT2RP2004095

F-NT2RP2004732

F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.18//18//55  
//Q48251

F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A  
DENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003

F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180  
//28//P32323

F-NT2RP2005882

F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//3  
9//P39217

F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULA  
TORY PROTEIN ALGR3).//0.00035//127//31//P15276

F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P0  
5204

F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX  
-1) (FRAGMENT).//0.064//110//34//P39881

F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRA  
GMENT).//0.020//95//29//P15583

F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.  
8e-05//165//29//P17437

F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: P  
EPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162

F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEI  
N).//0.38//124//31//P28284

F-OVARC1001029

F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377

F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN)  
(IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35)  
(CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845

F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRE  
SSOR SKC1).//3.2e-08//205//24//P53046

F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P0  
1668

【 0 8 3 1 】

相同性検索結果データ 8.

実施例 1 6 で選抜した54クローンの5'末端クローン配列に対するESTとSTSを除  
いたGenBank相同性検索結果データ

各データは、クローン配列名、トップヒットデータのDefinition、P値:比較配  
列の長さ (base):相同性(%), トップヒットデータのAccession No.の順に//で区  
切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000497

F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, L  
eu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710

F-HEMBA1003854//Homo sapiens clone RG270D13, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 18 unordered pieces.//1.7e-05//412//61//AC005081

F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//

0.77//466//59//AC002386

F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt] .//2.9e-47//341//77//S54641

F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13 .1-13.2, complete sequence.//0.28//436//59//Z83851

F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738

F-HEMBA1006406//HS\_2268\_B2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566

F-HEMBA1006650//H.sapiens CpG island DNA genomic MseI fragment, clone 5h 5, forward read cpg5h5.fl1a.//9.4e-24//143//96//Z55730

F-HEMBA1006812//X.laevis xUBFalpha1 mRNA for upstream binding factor 2.//0.96//234//64//X59863

F-HEMBB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 235 OH6, genomic survey sequence.//1.1e-68//375//94//AQ059158

F-HEMBB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760

F-HEMBB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127

F-MAMMA1001252

F-MAMMA1002094//H.sapiens CpG island DNA genomic MseI fragment, clone 18 4g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993

F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136

F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//24

5//61//D42108

F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199

F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961

F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411

F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//0.00013//121//76//AC005670

F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827

F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812

F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622

F-NT2RP2001214

F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189

F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589

F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094

F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10 q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 1 ordered pieces.//0.032//141//70//AC006097

F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.//1.8e-22//377//69//AP000018

F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050



F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476

F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233

F-NT2RP2004095//HS\_3083\_A1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698

F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631 P16, genomic survey sequence.//2.3e-20//120//99//B79035

F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970

F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410

F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770

F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652

F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242

F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775

F-NT2RP3001723//H.sapiens CpG island DNA genomic MseI fragment, clone 13g5, reverse read cp13g5.rt1a.//2.2e-18//163//85//Z56771

F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.3e-76//351//86//AC005180

F-NT2RP3003155

F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

F-OVARC1000008////0.0040//674//57//M82836

F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3

for transcriptional activator IE175 (= ICP 4).//1.1e-07//519//59//X06461  
F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221

F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1  
-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769

F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427

F-PLACE1003030

F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081

F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENC  
ING IN PROGRESS \*\*\*, in unordered pieces.//3.1e-39//214//98//AL031660

【 0 8 3 2 】

相同性検索結果データ 9.

実施例 1 6 で選抜した54クローンの3'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは、クローン配列名、トップヒットデータのDefinition、P値:比較配列の長さ (base):相同性(%), トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000497//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence  
./1.4e-38//185//84//U14567

R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//  
1.7e-07//399//59//D31785

R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1  
-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene

for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, ST  
Ss, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL03128  
1

R-HEMBA1004193//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence  
.//1.1e-34//188//81//U14567

R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Canc  
er Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC  
004241

R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complet-  
e sequence.//3.1e-21//341//67//AJ010598

R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequ  
ence.//1.7e-24//307//71//AC004678

R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cy  
clase.//0.76//246//62//X63282

R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.2  
2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an  
STS, complete sequence.//1.3e-31//297//77//AL023574

R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, compl  
ete sequence.//1.8e-15//350//65//AC003071

R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, \*\*\* SEQUENCI  
NG IN PROGRESS \*\*\*, in unordered pieces.//1.8e-55//430//81//Z82207

R-HEMBA100672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequ  
ence.//9.1e-39//437//71//AC006166

R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete  
sequence.//1.5e-37//275//85//AC004593

R-HEMBA1001871//Plasmodium falciparum chromosome 12 clone 3D7, \*\*\* SEQUE  
NCING IN PROGRESS \*\*\*, 5 unordered pieces.//0.00097//410//59//AC004688

R-MAMMA1001252//Homo sapiens clone 201104, \*\*\* SEQUENCING IN PROGRESS \*\*  
\*, 4 unordered pieces.//2.9e-13//364//64//AC004529

R-MAMMA1002094//HS\_3163\_A1\_A09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1.6e-21//283//73//AC005258

R-NT2RM4000657

R-NT2RM4000783

R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073

R-NT2RM4001178

R-NT2RM4002420

R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 complete genomic sequence, complete sequence.//0.58//108//67//AC002307

R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//D30043

R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//0.0058//166//69//AC005324

R-NT2RP2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Varlp (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822

R-NT2RP2001460

R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228

R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome X p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181

R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168

R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DX

S366 and DXS87 on chromosome X \*.//5.3e-39//449//72//Z81014  
R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete  
sequence.//0.0097//498//59//AC005412  
R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238  
301, genomic survey sequence.//1.2e-32//344//75//AQ196754  
R-NT2RP2003799///3.6e-05//408//60//AL010237  
R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, \*\*\* SEQUE  
NCING IN PROGRESS \*\*\*, in unordered pieces.//2.1e-10//455//61//AL034557  
R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.  
2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GS  
Ss, complete sequence.//5.1e-51//383//74//AL031287  
R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), c  
omplete sequence.//0.062//315//61//AC005219  
R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 conta  
ins flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repea  
t, CpG island, CpG island genomic fragments.//0.75//246//63//Z86062  
R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14; comple  
te sequence.//0.91//232//61//AC005232  
R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, c  
omplete sequence.//1.3e-19//405//66//U37368  
R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-0  
9//533//60//Z97348  
R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.0002  
6//499//58//AL034560  
R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//  
0.00035//337//61//AC002466  
R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete  
sequence.//1.8e-44//307//86//AC005180  
R-NT2RP3003155

R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6,  
genomic survey sequence.//0.95//95//65//B21351

R-OVARC1000008

R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequ  
ence.//0.91//83//71//AC005161

R-OVARC1000751//HS\_2222\_A2\_C09\_MR CIT Approved Human Genomic Sperm Libra  
ry D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey  
sequence.//2.8e-12//176//72//AQ033143

R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore  
X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) comple  
te sequence.//1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete  
sequence.//6.2e-52//514//75//AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subu  
nit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

R-PLACE1005549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon  
e: K19P17, complete sequence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENC  
ING IN PROGRESS \*\*\*, in unordered pieces.//1.1e-88//497//91//AL031660

【 0 8 3 3 】

相同性検索結果データ 1 0 .

実施例 1 6 で選抜した54クローンの5'末端クローン配列に対するHuman Unigen  
e相同性検索結果データ

各データは、クローン配列名、トップヒットデータのTitle、P値:比較配列の  
長さ (base):相同性(%), トップヒットデータのAccession No.の順に//で区切っ  
て記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000497//ou15a11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone I  
MAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element;; mRNA sequence.//3.7e-06//140//70//AA749151

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt] .//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element;; mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN. ;, mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

F-HEMBA1006812//zh49f01.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBA100672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH ;, mRNA sequence.//1.2e-16//117//92//AI580023

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

F-NT2RM4000634//DKFZp434D1813\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//L11329

F-NT2RM4002420//wg39f11.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element ;, mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997

F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence.//5.0e-07//116//71//AA017066

F-NT2RP2000660//qx01g11.x1 NCI\_CGAP\_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence.//0.027//120//65//AI225283

F-NT2RP2001214

F-NT2RP2001460//wb50h10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence.//0.0013//89//78//AI651878

F-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ;, mRNA sequence.//2.3e-18//120//93//AA427992

F-NT2RP2002056//tw44g09.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element;;, mRNA sequence.//2.



4e-07//99//79//AI811687

F-NT2RP2002677

F-NT2RP2002755//zj83d10.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element ;, mRNA sequence.//1.9e-19//229//76//AA705059

F-NT2RP2002843//wt88d12.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR:P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN. ;, mRNA sequence.//8.2e-15//314//67//AI964055

F-NT2RP2003101//wi65a03.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI763133

F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979

F-NT2RP2004095

F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691

F-NT2RP2004920//wz68d10.x1 NCI\_CGAP\_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR:000172 000172 LINE-1 REVERSE TRANSCRIPTASE ;, mRNA sequence.//0.0020//220//61//AI969546

F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194

F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770

F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence.//2.0e-05//385//62//Z78328

F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362

F-NT2RP3001282

F-NT2RP3001723//ws73d05.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 TAR1 repetitive element ;, mRNA sequence.//2.6e-07//245//66//AW008782

F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//64//R46086

F-NT2RP3003155

F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997

F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565

F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541

F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802

F-OVARC1001029//qv29c05.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ;, mRNA sequence.//0.0012//145//68//AI252422

F-PLACE1000814//ak42f05.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA868469

F-PLACE1003030

F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//1.2e-57//737//67//AJ010046

F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716

# 【 0 8 3 4 】

相同性検索結果データ 1 1.

実施例 1 6 で選抜した54クローンの3'末端クローン配列に対するHuman Unigen e相同性検索結果データ

各データは、クローン配列名、トップヒットデータのTitle、P値:比較配列の長さ (base):相同性(%)、トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないも

のは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

R-HEMBA1000497//np09h02.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains Alu repetitive element;contains element MER22 repetitive element ;, mRNA sequence.//6.2e-38//185//83//AA614254

R-HEMBA1001750//yy71b10.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:278971 3', mRNA sequence.//0.0045//193//63//N63303

R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//80//AL049263

R-HEMBA1004193//tr01e08.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.//1.5e-33//186//81//AI914747

R-HEMBA1004860//qh16b06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA sequence.//0.017//118//69//AI218308

R-HEMBA1005572//wj16h05.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA sequence.//4.6e-111//522//99//AI861830

R-HEMBA1006038//DKFZp434E1117\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5', mRNA sequence.//1.2e-22//295//72//AL041450

R-HEMBA1006092//qt30d09.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE:1949489 3' similar to contains element PTR5 repetitive element ;, mRNA sequence.//1.4e-87//422//98//AI337963

R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291//76//AB018295

R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630

R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087

R-HEMBA1000672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//74//AL096734

R-HEMBB1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar to contains Alu repetitive element;; mRNA sequence.//9.9e-44//275//88//AA410788

R-HEMBB1001871//wg20c02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321

R-MAMMA1001252//aa61h04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to contains Alu repetitive element;contains element XTR repetitive element ;, mRNA sequence.//9.0e-19//127//91//AA504355

R-MAMMA1002094//wd28h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mRNA sequence.//2.5e-68//328//99//AI936520

R-NT2RM4000634//DKFZp434F2016\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3', mRNA sequence.//8.2e-20//185//81//AL041146

R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992

R-NT2RM4000783

R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136

R-NT2RM4001178//tk08e03.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA sequence.//0.77//96//62//AI457506

R-NT2RM4002420//w158b04.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA sequence.//2.4e-85//438//94//AI857508

R-NT2RP2000198//nx19b11.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA sequence.//1.9e-45//270//91//AA738352

R-NT2RP2000551//tg80h11.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA sequence.//3.3e-53//311//85//AI417680

R-NT2RP2000660//ns42a06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA sequence.//4.3e-26//142//97//AA805691

R-NT2RP2001214//tw65g08.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains element MSR1 repetitive element ;, mRNA seq

uence.//1.5e-57//289//97//AI680174

R-NT2RP2001460

R-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDN  
A clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEI  
N ZFP-1 ;, mRNA sequence.//6.0e-13//85//96//AA427992

R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone  
IMAGE:130846 3', mRNA sequence.//0.0016//208//65//R22302

R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.  
4e-26//339//71//AB011096

R-NT2RP2002755//qd50d10.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA  
clone IMAGE:1732915 3', mRNA sequence.//1.5e-26//419//66//AI190698

R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone  
IMAGE:2373639 3' similar to contains L1.t1 L1 repetitive element ;, mRN  
A sequence.//1.8e-45//463//74//AI749673

R-NT2RP2003101//ty24h05.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:22  
80057 3', mRNA sequence.//7.5e-73//347//99//AI758824

R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0  
.0026//247//65//AB018294

R-NT2RP2004095//zv08c02.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAG  
E:753026 3' similar to contains element MER32 repetitive element ;, mRNA  
sequence.//9.6e-07//188//66//AA436455

R-NT2RP2004732//tu60a07.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2  
255412 3' similar to contains Alu repetitive element;contains element L1  
repetitive element ;, mRNA sequence.//4.3e-25//414//68//AI678956

R-NT2RP2004920//wd13h02.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:23  
28051 3', mRNA sequence.//6.8e-91//483//93//AI694022

R-NT2RP2005454//yy77g09.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapien  
s cDNA clone IMAGE:279616 3', mRNA sequence.//0.0070//325//59//N48302

R-NT2RP2005776//qq97d06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDN

A clone IMAGE:1939307 3', mRNA sequence.//7.5e-08//89//82//AI338419  
R-NT2RP2005806//wc29h01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:  
2316625 3' similar to contains MER2.b3 MER2 repetitive element ;, mRNA s  
equence.//3.2e-16//235//71//AI671398  
R-NT2RP2005882//wo31f09.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2  
456969 3', mRNA sequence.//0.00095//352//59//AI925528  
R-NT2RP3001282//wg35b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA  
clone IMAGE:2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199  
R-NT2RP3001723//wo48e06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2  
458594 3', mRNA sequence.//4.2e-98//471//98//AI926617  
R-NT2RP3002099//DKFZp564L227\_s1 564 (synonym: hfbr2) Homo sapiens cDNA c  
lone DKFZp564L227 3', mRNA sequence.//9.2e-50//329//87//AL037910  
R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapi  
ens cDNA clone IMAGE:595668 3', mRNA sequence.//1.4e-30//159//99//AA1731  
72  
R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR  
./0.43//66//75//AF035594  
R-OVARC1000008//wa69e12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone I  
MAGE:2301454 3', mRNA sequence.//1.0e-77//376//98//AI699393  
R-OVARC1000724//tf94b10.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2  
106907 3', mRNA sequence.//0.71//27//100//AI380236  
R-OVARC1000751//og93d04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1  
455847 3', mRNA sequence.//3.5e-13//274//63//AA863306  
R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clo  
ne IMAGE:290906 5' similar to contains Alu repetitive element;contains e  
lement PTR5 repetitive element ;, mRNA sequence.//3.5e-13//175//74//N994  
64  
R-PLACE1000814//tg49a08.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone I  
MAGE:2112086 3' similar to contains L1.t2 L1 L1 repetitive element ;, mR

NA sequence.//2.2e-18//285//69//AI424789

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//4.0e-34//225//90//AF032387

R-PLACE1005549//tm26b11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA sequence.//0.91//127//66//AI480253

R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5' similar to contains Alu repetitive element; contains LTR4 repetitive element ;, mRNA sequence.//2.4e-36//245//87//R92256

【 0 8 3 5 】

相同性検索結果データ 1 2.

全長塩基配列および推定アミノ酸配列に対する相同性検索結果データ

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//6.4E-99//457aa//45%//Q09996

C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344

C-HEMBA1000129//HYPOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//Q09884

C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738

C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221

C-HEMBA1000231

C-HEMBA1000264

C-HEMBA1000280

C-HEMBA1000282

C-HEMBA1000303// "Mus musculus Plenty of SH3s (POSH) mRNA, complete cds."//7.1E-254//1440bp//87%//AF030131

C-HEMBA1000333// "Homo sapiens mRNA for KIAA0874 protein, partial cds."//  
4.8E-253//1148bp//99%//AB020681

C-HEMBA1000351

C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp56  
6C243).//3.3E-287//815bp//98%//AL050274

C-HEMBA1000396

C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357

C-HEMBA1000442

C-HEMBA1000456

C-HEMBA1000504

C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490

C-HEMBA1000519

C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01  
755

C-HEMBA1000542// "Rattus norvegicus mRNA for dipeptidyl peptidase III, co  
mplete cds."//2.2E-194//663bp//83%//D89340

C-HEMBA1000545

C-HEMBA1000557

C-HEMBA1000592// "Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.  
"//0//1465bp//99%//AF121856

C-HEMBA1000594

C-HEMBA1000604

C-HEMBA1000622

C-HEMBA1000637

C-HEMBA1000655

C-HEMBA1000657// "Rattus norvegicus ADP-ribosylation factor-directed GTPa  
se activating protein mRNA, complete cds."//7.2E-156//1366bp//76%//U3577

6

C-HEMBA1000749



C-HEMBA1000769  
C-HEMBA1000773  
C-HEMBA1000774  
C-HEMBA1000822  
C-HEMBA1000843  
C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//11  
9aa//87%//P51689  
C-HEMBA1000870  
C-HEMBA1000908  
C-HEMBA1000934  
C-HEMBA1000972  
C-HEMBA1000986  
C-HEMBA1000991  
C-HEMBA1001008  
C-HEMBA1001059//”Human N-acetylgalactosamine 6-sulphatase (GALNS) gene,  
exon 14.”//4.8E-169//786bp//99%//U06088  
C-HEMBA1001094  
C-HEMBA1001302//”Homo sapiens calcium binding protein precursor, mRNA, c  
omplete cds.”//9.6E-258//682bp//94%//AF153686  
C-HEMBA1001330  
C-HEMBA1001497  
C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2)  
(VAMP-2).//2.3E-53//110aa//100%//P19065  
C-HEMBA1001570  
C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1  
.6E-166//506aa//60%//P42803  
C-HEMBA1001640  
C-HEMBA1001655  
C-HEMBA1001672//”Homo sapiens methyl-CpG binding domain-containing prote

in MBD3 (MBD3) mRNA, complete cds."//0//1707bp//98%//AF072247

C-HEMBA1001711

C-HEMBA1001723// "Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//4.7E-172//1240bp//81%//AF051155

C-HEMBA1001746// "Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//7.6E-59//998bp//64%//AF098066

C-HEMBA1001781

C-HEMBA1001804// "Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//1637bp//99%//AF125158

C-HEMBA1001822// "Mus musculus Ese2L protein mRNA, complete cds."//1.9E-235//1329bp//89%//AF132479

C-HEMBA1001824

C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332

C-HEMBA1001910

C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535

C-HEMBA1001921// "Homo sapiens germinal center kinase related protein kinase mRNA, complete cds."//0//1850bp//99%//AF000145

C-HEMBA1001939

C-HEMBA1001950// "Homo sapiens mRNA for KIAA0971 protein, complete cds."//0//1974bp//99%//AB023188

C-HEMBA1001967// "Homo sapiens NY-REN-57 antigen mRNA, partial cds."//0//1721bp//99%//AF155114

C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089

C-HEMBA1002092// "Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds."//1.3E-271//1583bp//88%//U92703

C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357

C-HEMBA1002150

C-HEMBA1002151// "Rattus norvegicus p34 mRNA, complete cds."//1.1E-153//1059bp//82%//AF178669

C-HEMBA1002189

C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]//2.2E-199//392aa//89%//P47226

C-HEMBA1002229

C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087

C-HEMBA1002341// "Homo sapiens mRNA for KIAA0771 protein, partial cds."//0//1514bp//99%//AB018314

C-HEMBA1002417// "Homo sapiens chromosome 19, cosmid R28784, complete sequence."//1.4E-299//294bp//100%//AC005954

C-HEMBA1002547// "Homo sapiens agrin precursor mRNA, partial cds."//0//1605bp//97%//AF016903

C-HEMBA1002703

C-HEMBA1002779

C-HEMBA1002816

C-HEMBA1002970

C-HEMBA1002999// "Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds."//1.4E-171//1552bp//75%//U20286

C-HEMBA1003021

C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014

C-HEMBA1003079

C-HEMBA1003273

C-HEMBA1003304

C-HEMBA1003309

C-HEMBA1003376

C-HEMBA1003384

C-HEMBA1003531

C-HEMBA1003548  
C-HEMBA1003556  
C-HEMBA1003571  
C-HEMBA1003579  
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//  
32%//Q13105  
C-HEMBA1003692  
C-HEMBA1003720  
C-HEMBA1003725  
C-HEMBA1003729  
C-HEMBA1003758  
C-HEMBA1003773//”Mus musculus signal recognition particle receptor beta  
subunit mRNA, complete cds.”//5.8E-81//511bp//86%//U17343  
C-HEMBA1003783//”Mus musculus bromodomain-containing protein BP75 mRNA,  
complete cds.”//1.1E-190//1204bp//84%//AF084259  
C-HEMBA1003799  
C-HEMBA1003804  
C-HEMBA1003805//”Mus musculus KH domain RNA binding protein QKI-5A mRNA,  
complete cds.”//0//988bp//95%//AF090402  
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40  
484  
C-HEMBA1003856  
C-HEMBA1003866//”Mus musculus semaphorin VIa mRNA, complete cds.”//1.2E-  
105//1192bp//70%//AF030430  
C-HEMBA1003879  
C-HEMBA1003880  
C-HEMBA1003893  
C-HEMBA1003908  
C-HEMBA1003937

C-HEMBA1003942  
C-HEMBA1003958  
C-HEMBA1003976  
C-HEMBA1003978// "Homo sapiens mRNA for KIAA0840 protein, partial cds."//  
0//1530bp//100%//AB020647  
C-HEMBA1003985  
C-HEMBA1004011  
C-HEMBA1004024  
C-HEMBA1004038  
C-HEMBA1004045  
C-HEMBA1004048  
C-HEMBA1004111// "Homo sapiens mRNA for KIAA1276 protein, partial cds."//  
1.00E-163//751bp//99%//AB033102  
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q141  
41  
C-HEMBA1004138  
C-HEMBA1004143  
C-HEMBA1004150  
C-HEMBA1004168// "Homo sapiens geminin mRNA, complete cds."//3.9E-208//95  
1bp//99%//AF067855  
C-HEMBA1004200  
C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153  
C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991  
C-HEMBA1004238  
C-HEMBA1004248// "Homo sapiens insulin induced protein 2 mRNA, complete c  
ds."//8.20E-175//552bp//97%//AF125392  
C-HEMBA1004272  
C-HEMBA1004274  
C-HEMBA1004275// "Homo sapiens mRNA for KIAA1111 protein, partial cds."//

0//1341bp//99%//AB029034

C-HEMBA1004286//”Homo sapiens TGF beta receptor associated protein-1 mRN  
A, complete cds.”//0//1982bp//99%//AF022795

C-HEMBA1004312

C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%  
//Q99676

C-HEMBA1004323

C-HEMBA1004327

C-HEMBA1004330

C-HEMBA1004341

C-HEMBA1004366

C-HEMBA1004372

C-HEMBA1004389//”Homo sapiens zinc finger DNA binding protein 99 (ZNF281  
) mRNA, complete cds.”//0//1437bp//99%//AF125158

C-HEMBA1004394

C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPI  
ASE) (ROTAMASE) (CYCLOPHILIN-10).//3.2E-32//148aa//52%//P52017

C-HEMBA1004429

C-HEMBA1004460

C-HEMBA1004461

C-HEMBA1004502

C-HEMBA1004554

C-HEMBA1004560

C-HEMBA1004610

C-HEMBA1004629

C-HEMBA1004632

C-HEMBA1004637

C-HEMBA1004670

C-HEMBA1004672

C-HEMBA1004697

C-HEMBA1004711

C-HEMBA1004725

C-HEMBA1004730

C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743

C-HEMBA1004751

C-HEMBA1004752

C-HEMBA1004889//”Human C3f mRNA; complete cds.”//6.70E-24//341aa//26%//U72515

C-HEMBA1004934

C-HEMBA1004944

C-HEMBA1004973

C-HEMBA1004977

C-HEMBA1005009//”Homo sapiens BAF53a (BAF53a) mRNA, complete cds.”//0//1813bp//99%//AF041474

C-HEMBA1005083

C-HEMBA1005113

C-HEMBA1005133

C-HEMBA1005185

C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929

C-HEMBA1005252//”Homo sapiens mRNA for KIAA0585 protein, partial cds.”//1.2E-268//1215bp//99%//AB011157

C-HEMBA1005296

C-HEMBA1005314

C-HEMBA1005331

C-HEMBA1005394

C-HEMBA1005403

C-HEMBA1005423// "Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)  
mRNA, complete cds."//2E-213//537bp//99%//AF041248

C-HEMBA1005468

C-HEMBA1005469

C-HEMBA1005474

C-HEMBA1005517

C-HEMBA1005518

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//  
Q60809

C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929

C-HEMBA1005576// "Homo sapiens mRNA for KIAA0463 protein, partial cds."//  
1.1E-181//835bp//99%//AB007932

C-HEMBA1005582// "TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYT  
OSKELETAL TROPOMYOSIN)."//0.00000009//213aa//27%//P09492

C-HEMBA1005583

C-HEMBA1005595// "DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)."//2.3E-54//562aa/  
/29%//P34036

C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp56  
4K133).//2.2e-315//1448bp//99%//AL050012

C-HEMBA1005621// "Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds."  
//2.9E-224//1031bp//99%//AF139365

C-HEMBA1005666

C-HEMBA1005680

C-HEMBA1005685

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY  
SUBUNIT).//4.4E-17//167aa//34%//P25296

C-HEMBA1005746

C-HEMBA1005755

C-HEMBA1005813



C-HEMBA1005822  
C-HEMBA1005834  
C-HEMBA1005884  
C-HEMBA1005891  
C-HEMBA1005909  
C-HEMBA1005911  
C-HEMBA1005931  
C-HEMBA1005963  
C-HEMBA1005991  
C-HEMBA1006005  
C-HEMBA1006031// "Homo sapiens mRNA for putative phospholipase, complete  
cds."//0//1413bp//99%//AB019435  
C-HEMBA1006067  
C-HEMBA1006081  
C-HEMBA1006091  
C-HEMBA1006100  
C-HEMBA1006108// "Homo sapiens mRNA for KIAA0943 protein, partial cds."//  
4.8E-245//764bp//99%//AB023160  
C-HEMBA1006121  
C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794  
C-HEMBA1006155  
C-HEMBA1006158// "Homo sapiens transcription factor forkhead-like 7 (FKHL  
7) gene, complete cds."//0//1551bp//99%//AF048693  
C-HEMBA1006182  
C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39  
%/P05142  
C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%/  
/AF070557  
C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//

0.00000002//62aa//53%/P42698  
 C-HEMBA1006259  
 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)//1.3E-123//20  
 0aa//73%/P10265  
 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A  
 DENYLYLTRANSFERASE)//1E-210//490aa//77%/P25500  
 C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2//0.0000  
 00012//176aa//30%/P32505  
 C-HEMBA1006284  
 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//4.2E-12//21  
 5aa//23%/P70473  
 C-HEMBA1006293  
 C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REG  
 ION//1.4E-48//248aa//43%/P38821  
 C-HEMBA1006349  
 C-HEMBA1006364  
 C-HEMBA1006381  
 C-HEMBA1006398//”Human L1 element L1.6 putative p150 gene, complete cds.  
 ”//2E-277//1729bp//85%/U93563  
 C-HEMBA1006445//”Homo sapiens putative tumor supressor NOEY2 mRNA, compl  
 ete cds.”//1.4E-270//1224bp//100%/U96750  
 C-HEMBA1006483  
 C-HEMBA1006492  
 C-HEMBA1006497  
 C-HEMBA1006502  
 C-HEMBA1006507//”Homo sapiens mRNA for KIAA0666 protein, partial cds.”//  
 0//2334bp//99%/AB014566  
 C-HEMBA1006535  
 C-HEMBA1006559//”Mus musculus PRAJA1 (Praj1) mRNA, complete cds.”//2.8E

-206//1107bp//83%/U06944

C-HEMBA1006566

C-HEMBA1006579

C-HEMBA1006583

C-HEMBA1006612

C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.000

00069//109aa//38%/Q58323

C-HEMBA1006643

C-HEMBA1006674

C-HEMBA1006682

C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN

IN PMC1-TFG2 INTERGENIC REGION.//3.3E-22//241aa//31%/P53196

C-HEMBA1006717

C-HEMBA1006744

C-HEMBA1006754

C-HEMBA1006767

C-HEMBA1006789

C-HEMBA1006832

C-HEMBA1006885// "Homo sapiens gene for Proline synthetase associated, complete cds."//0//1467bp//96%/AB018566

C-HEMBA1006900

C-HEMBA1006926

C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.

//1.8E-226//1039bp//99%/AJ010841

C-HEMBA1006973// "Homo sapiens rab3-GAP regulatory domain mRNA, complete cds."//5.6E-143//740bp//94%/AF004828

C-HEMBA1006993

C-HEMBA1007002

C-HEMBA1007062

C-HEMBA1007080

C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626

C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%//AL117450

C-HEMBA1007194// "Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds."//0//1588bp//99%//AF139658

C-HEMBA1007206

C-HEMBA1007256

C-HEMBA1007267

C-HEMBA1007281

C-HEMBA1007300// "Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds."//0//1519bp//99%//AF127479

C-HEMBA1007301

C-HEMBA1007319

C-HEMBA1007320

C-HEMBA1007327

C-HEMBA1007347

C-HEMBA1000005

C-HEMBA1000030

C-HEMBA1000048

C-HEMBA1000099

C-HEMBA1000141

C-HEMBA1000198

C-HEMBA1000217// "Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds."//0//1038bp//99%//AF090385

C-HEMBA1000218

C-HEMBA1000274

C-HEMBA1000312

C-HEMBB1000402  
 C-HEMBB1000420  
 C-HEMBB1000480  
 C-HEMBB1000530  
 C-HEMBB1000550  
 C-HEMBB1000556//”Homo sapiens mRNA for KIAA0750 protein, complete cds.”/  
 /6.3E-74//1213bp//64%//AB018293  
 C-HEMBB1000586  
 C-HEMBB1000592  
 C-HEMBB1000593//”Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA,  
 complete cds.”//1.3E-107//503bp//99%//AF067864  
 C-HEMBB1000649  
 C-HEMBB1000693//”Homo sapiens neuroanl mRNA, complete cds.”//0//2952bp//  
 94%//AF040723  
 C-HEMBB1000822  
 C-HEMBB1000826  
 C-HEMBB1000890  
 C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-)./  
 /1.10E-08//129aa//31%//P29122  
 C-HEMBB1001008  
 C-HEMBB1001020//”Homo sapiens mRNA for KIAA0889 protein, complete cds.”/  
 /0//1812bp//98%//AB020696  
 C-HEMBB1001051  
 C-HEMBB1001112//”Homo sapiens sec61 homolog mRNA, complete cds.”//6E-145  
 //961bp//83%//AF077032  
 C-HEMBB1001221  
 C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//5  
 4%//P46938  
 C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)./

/7E-43//394aa//34%/P16157

C-HEMBB1001302

C-HEMBB1001335

C-HEMBB1001337

C-HEMBB1001356

C-HEMBB1001364

C-HEMBB1001366

C-HEMBB1001367

C-HEMBB1001527

C-HEMBB1001537

C-HEMBB1002359

C-HEMBB1002415

C-HEMBB1002457

C-HEMBB1002492

C-HEMBB1002495

C-HEMBB1002502

C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%/P27544

C-HEMBB1002600// "Homo sapiens tetraspan NET-5 mRNA, complete cds."//0//1  
417bp//99%/AF089749

C-HEMBB1002607// "Homo sapiens vitamin D3 receptor interacting protein (D  
RIP80) mRNA, complete cds."//2E-136//660bp//98%/AF105421

C-HEMBB1002684

C-HEMBB1002692

C-HEMBB1002697

C-HEMBB1002705// "Homo sapiens CGI-27 protein mRNA, complete cds."//7.80E  
-285//841bp//96%/AF132961

C-MAMMA1000019

C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM  
05).//8.2E-198//868bp//99%/Z47553

C-MAMMA1000025  
C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]../1.5E-90//3  
23aa//48%//P47226  
C-MAMMA1000069  
C-MAMMA1000084  
C-MAMMA1000139  
C-MAMMA1000163  
C-MAMMA1000171  
C-MAMMA1000173//”Homo sapiens src homology 3 domain-containing protein H  
IP-55 mRNA, complete cds.”//2.6E-164//1044bp//87%//AF197060  
C-MAMMA1000277  
C-MAMMA1000278  
C-MAMMA1000284//P.walti mRNA for rnp associated protein 55../2.2E-109//8  
64bp//76%//X99836  
C-MAMMA1000309  
C-MAMMA1000312  
C-MAMMA1000313  
C-MAMMA1000361  
C-MAMMA1000388//”Homo sapiens UKLF mRNA for ubiquitous Kruppel like fact  
or, complete cds.”//0//1466bp//99%//AB015132  
C-MAMMA1000395  
C-MAMMA1000410  
C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./  
/2.00E-30//119aa//53%//Q09232  
C-MAMMA1000421  
C-MAMMA1000422  
C-MAMMA1000468  
C-MAMMA1000472  
C-MAMMA1000490

C-MAMMA1000524

C-MAMMA1000567

C-MAMMA1000612// "Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//1E-95//1115bp//72%//AF051155

C-MAMMA1000623

C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365

C-MAMMA1000664

C-MAMMA1000670

C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//4.4E-33//250aa//33%//P42660

C-MAMMA1000713//L-RIBULOXINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524

C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1E-77//395aa//45%//O14646

C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779

C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//55%//P87115

C-MAMMA1000746

C-MAMMA1000775

C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500

C-MAMMA1000831

C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.8E-40//101aa//54%//O27540

C-MAMMA1000842

C-MAMMA1000843

C-MAMMA1000856

C-MAMMA1000865

C-MAMMA1000875



C-MAMMA1000906  
C-MAMMA1000908  
C-MAMMA1000914  
C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//  
AJ250711  
C-MAMMA1000968  
C-MAMMA1000979  
C-MAMMA1001008//”Homo sapiens aspartic-like protease mRNA, complete cds.  
”//2.50E-276//1263bp//99%//AF117892  
C-MAMMA1001021  
C-MAMMA1001041//”SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BET  
A CHAIN) (FODRIN BETA CHAIN) (SPTBN1).”//1.6E-16//113aa//41%//Q01082  
C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99  
%//AJ237946  
C-MAMMA1001075//”Homo sapiens CGI-72 protein mRNA, complete cds.”//1.3E-  
181//397bp//98%//AF151830  
C-MAMMA1001078  
C-MAMMA1001091  
C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P  
51521  
C-MAMMA1001110  
C-MAMMA1001126  
C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273  
C-MAMMA1001143  
C-MAMMA1001154  
C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q9  
2338  
C-MAMMA1001215  
C-MAMMA1001244

C-MAMMA1001259//”Mus musculus F-box protein FBX18 mRNA, partial cds.”//2  
 .3E-271//1414bp//89%//AF184275  
 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III./  
 /2.1E-52//630aa//30%//P34537  
 C-MAMMA1001343  
 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp5  
 6400823).//0//2131bp//99%//AL080121  
 C-MAMMA1001419  
 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE)  
 (FRAGMENT).//6.5E-129//260aa//92%//P52623  
 C-MAMMA1001510  
 C-MAMMA1001522  
 C-MAMMA1001576//”Human gamma-tubulin mRNA, complete cds.”//7.5E-276//156  
 1bp//90%//M61764  
 C-MAMMA1001604  
 C-MAMMA1001620  
 C-MAMMA1001635  
 C-MAMMA1001649  
 C-MAMMA1001686  
 C-MAMMA1001692  
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8  
 .5E-32//171aa//36%//P21573  
 C-MAMMA1001754//”Homo sapiens CGI-11 protein mRNA, complete cds.”//0//18  
 37bp//98%//AF132945  
 C-MAMMA1001757  
 C-MAMMA1001764  
 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45/  
 /351aa//38%//Q58556  
 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79

%//X85991

C-MAMMA1001790

C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q  
07230

C-MAMMA1001858

C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793

C-MAMMA1001970

C-MAMMA1002042

C-MAMMA1002068

C-MAMMA1002153

C-MAMMA1002156

C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//  
157aa//70%//P15880

C-MAMMA1002174

C-MAMMA1002209

C-MAMMA1002219//”Homo sapiens mRNA for KIAA1067 protein, partial cds.”//  
1.1E-181//861bp//98%//AB028990

C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-  
2B GDP-GTP EXCHANGE FACTOR).//8.8E-217//310aa//86%//P70541

C-MAMMA1002243

C-MAMMA1002268//”Mus musculus sphingosine kinase (SPHK1a) mRNA, partial  
cds.”//1E-190//1624bp//76%//AF068748

C-MAMMA1002269

C-MAMMA1002292

C-MAMMA1002294

C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1  
.1E-214//881bp//97%//AJ011679

C-MAMMA1002312

C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%/

/X85991

C-MAMMA1002333

C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%/P  
40882

C-MAMMA1002353

C-MAMMA1002355

C-MAMMA1002356

C-MAMMA1002362

C-MAMMA1002380

C-MAMMA1002384

C-MAMMA1002427

C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).  
//1E-11//128aa//36%/P47623

C-MAMMA1002485//”Homo sapiens stanniocalcin-related protein mRNA, complete cds.”//0//1822bp//99%/AF098462

C-MAMMA1002494

C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.2E-34//337aa//31%/P43571

C-MAMMA1002530//”Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.”//0//1910bp//99%/AF065214

C-MAMMA1002554

C-MAMMA1002585//”Homo sapiens mRNA for KIAA0860 protein, complete cds.”/  
/0//1405bp//99%/AB020667

C-MAMMA1002598

C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//9.5E-16//159aa//37%/Q09931

C-MAMMA1002655//”Homo sapiens mRNA for ganglioside sialidase, complete cds.”//0//1515bp//99%/AB008185

C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA  
LIGASE) (ACYL- ACTIVATING ENZYME).//1.1E-45//618aa//26%//P27550  
C-MAMMA1002673  
C-MAMMA1002684//”Homo sapiens mRNA for KIAA0214 protein, complete cds.”/  
/0//3174bp//99%//D86987  
C-MAMMA1002711  
C-MAMMA1002769//”Homo sapiens cell cycle progression restoration 8 prote  
in (CPR8) mRNA, complete cds.”//2.2E-25//330bp//77%//AF011794  
C-MAMMA1002775  
C-MAMMA1002782  
C-MAMMA1002796  
C-MAMMA1002807  
C-MAMMA1002838  
C-MAMMA1002842//”Mus musculus c-Cbl associated protein CAP mRNA, complet  
e cds.”//2.6E-58//373bp//81%//U58883  
C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTE  
IN).//1.4E-160//305aa//85%//P48059  
C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5  
.7E-30//214aa//35%//P48060  
C-MAMMA1002886  
C-MAMMA1002890  
C-MAMMA1002938//”Homo sapiens mRNA for KIAA0698 protein, complete cds.”/  
/8.4E-252//1139bp//100%//AB014598  
C-MAMMA1002964  
C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.7E-123//370aa//66%//Q02874  
C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.4E-46//332aa//36%//  
P06746  
C-MAMMA1003015  
C-MAMMA1003019

C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2  
.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//  
33%/P23851

C-MAMMA1003039

C-MAMMA1003044

C-MAMMA1003049

C-MAMMA1003056

C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%/Q60584

C-MAMMA1003066

C-MAMMA1003099

C-MAMMA1003104

C-MAMMA1003113//”Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, com  
plete cds.”//1.1E-234//1178bp//86%/AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%/P4673  
5

C-MAMMA1003135

C-MAMMA1003146//Homo sapiens mRNA for GALT3 protein.//4.3E-218//996bp//9  
9%/Y15062

C-MAMMA1003150//”Homo sapiens mRNA for KIAA1096 protein, partial cds.”//  
0//1342bp//99%/AB029019

C-MAMMA1003166//”Homo sapiens MLL septin-like fusion protein (MSF) mRNA,  
complete cds.”//3.10E-158//592bp//97%/AF123052

C-NT2RM1000032

C-NT2RM1000035//”Human mRNA for KIAA0199 gene, partial cds.”//0//2948bp/  
/99%/D83782

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REG  
ION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%/P37596

C-NT2RM1000055//”Homo sapiens mRNA for KIAA0829 protein, partial cds.”//  
0//3111bp//99%/AB020636

C-NT2RM1000059

C-NT2RM1000062

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%/P87072

C-NT2RM1000119

C-NT2RM1000127

C-NT2RM1000131//”Homo sapiens mRNA for KIAA0792 protein, complete cds.”//0//2980bp//99%/AB018335

C-NT2RM1000132//”Homo sapiens NADH:ubiquinone oxidoreductase NDUF5 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.”//7.8E-110//516bp//99%/AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-38//469aa//27%/P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%/P87072

C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.1E-10//94aa//47%/042643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%/AJ245820

C-NT2RM1000244//”Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.”//2E-126//592bp//99%/U81002

C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%/X73882

C-NT2RM1000256//”Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.”//0//3012bp//99%/AB016789

C-NT2RM1000260//”Human mRNA for KIAA0130 gene, complete cds.”//0//3139bp//98%/D50920

C-NT2RM1000271

C-NT2RM1000300

C-NT2RM1000314//”Human mRNA for KIAA0159 gene, complete cds.”//0//4349bp

//99%//D63880

C-NT2RM1000354// "Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//7.4E-245//2101bp//68%//AF111423

C-NT2RM1000355// "Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds."//0//1599bp//99%//AF152462

C-NT2RM1000365

C-NT2RM1000377// "Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds."//3.2E-196//1016bp//94%//AF179212

C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000019//67aa//31%//P53915

C-NT2RM1000399

C-NT2RM1000430// "Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."//1.4E-185//1486bp//81%//AF084928

C-NT2RM1000555// "Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%//AB020692

C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372

C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636

C-NT2RM1000661// "Homo sapiens translation initiation factor 4e mRNA, complete cds."//4.3E-210//960bp//99%//AF038957

C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989

C-NT2RM1000672

C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440

C-NT2RM1000699

C-NT2RM1000741// "Homo sapiens mRNA for KIAA0567 protein, partial cds."//1.1E-295//1338bp//99%//AB011139

C-NT2RM1000742// "Homo sapiens AC133 antigen mRNA, complete cds."//0//352



4bp//99%//AF027208

C-NT2RM1000746//”Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.”//6.70E-227//1043bp//99%//AF141310

C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202

C-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808

C-NT2RM1000780

C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//1.1E-98//571bp//89%//Z97207

C-NT2RM1000802

C-NT2RM1000811//”Homo sapiens AC133 antigen mRNA, complete cds.”//0//3524bp//99%//AF027208

C-NT2RM1000826//”Homo sapiens mRNA for KIAA0885 protein, complete cds.”//0//2885bp//99%//AB020692

C-NT2RM1000829

C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//P16157

C-NT2RM1000852//”Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.”//0//2206bp//99%//AF077033

C-NT2RM1000857//”Homo sapiens mRNA for KIAA0962 protein, partial cds.”//0//3716bp//99%//AB023179

C-NT2RM1000874//”Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.”//1.4E-244//1113bp//99%//AF043733

C-NT2RM1000882//”Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.”//4.30E-122//1394bp//69%//AF126799

C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa//30%//P34537

C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700

C-NT2RM1000898// "ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR)."//8.9E-26//22  
9aa//29%//P02583

C-NT2RM1000905// "Homo sapiens HSPC021 mRNA, complete cds."//0//1480bp//9  
9%//AF077207

C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.  
//1E-15//266aa//26%//P46577

C-NT2RM1000927

C-NT2RM1000962

C-NT2RM1000978

C-NT2RM1001003// "Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA,  
complete cds."//0//2230bp//99%//AF030233

C-NT2RM1001043

C-NT2RM1001066

C-NT2RM1001072// "1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERA  
SE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II  
) (PLC-148)."//8.3E-47//259aa//35%//P08487

C-NT2RM1001085// "Rattus norvegicus brain specific cortactin-binding prot  
ein CBP90 mRNA, partial cds."//3.7E-32//460bp//64%//AF053768

C-NT2RM1001102// "Human HEM45 mRNA, complete cds."//2.3E-27//482bp//63%//  
U88964

C-NT2RM1001105

C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp5  
64F0522).//0//1756bp//99%//AL049943

C-NT2RM2000420

C-NT2RM2000566// "Homo sapiens integrin alpha-7 mRNA, complete cds."//0//  
2519bp//96%//AF032108

C-NT2RM2000609

C-NT2RM2000612// "Rattus norvegicus ADP-ribosylation factor-directed GTPa  
se activating protein mRNA, complete cds."//2.6E-106//1069bp//74%//U3577

6

C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//2  
49aa//73%//P28160

C-NT2RM2001588

C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ  
132440

C-NT2RM2001613//"Homo sapiens sec61 homolog mRNA, complete cds."//0//260  
1bp//99%//AF084458

C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844

C-NT2RM2001648//"Homo sapiens sec61 homolog mRNA, complete cds."//0//242  
1bp//99%//AF084458

C-NT2RM2001652//"Homo sapiens guanine nucleotide exchange factor mRNA, c  
omplete cds."//0//2608bp//99%//AF111162

C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P  
20107

C-NT2RM2001664//"Homo sapiens IkappaB kinase complex associated protein  
(IKAP) mRNA, complete cds."//0//2471bp//99%//AF044195

C-NT2RM2001668//"Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alter  
native splice product ending in intron 11, complete cds."//6.2E-16//464b  
p//62%//AF083391

C-NT2RM2001671//"Oryctolagus cuniculus sarcolemmal associated protein (S  
LAP1) mRNA, complete cds."//0//1843bp//94%//U21155

C-NT2RM2001675

C-NT2RM2001681

C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//  
4.60E-20//253aa//30%//Q09674

C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF  
103804

C-NT2RM2001696

C-NT2RM2001698// "Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//6.2E-253//1170bp//99%//AB028600

C-NT2RM2001700// "ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT)."//5.7E-130//536aa//49%//P50544

C-NT2RM2001716

C-NT2RM2001723

C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//7.2E-16//381aa//27%//Q09931

C-NT2RM2001743// "Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds."//0//1498bp//99%//AF011792

C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.8E-11//119aa//36%//Q92609

C-NT2RM2001760// "Homo sapiens sec61 homolog mRNA, complete cds."//0//2379bp//99%//AF084458

C-NT2RM2001768

C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154//394aa//64%//P52742

C-NT2RM2001782// "Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds."//0//1470bp//99%//AF135422

C-NT2RM2001784

C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp//99%//AL050118

C-NT2RM2001813

C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39%//P32657

C-NT2RM2001839// "Homo sapiens calumein (Calu) mRNA, complete cds."//0//2415bp//97%//AF013759

C-NT2RM2001840

C-NT2RM2001855

C-NT2RM2001867// "Homo sapiens mRNA for KIAA0943 protein, partial cds."//

0//967bp//99%//AB023160

C-NT2RM2001879

C-NT2RM2001983// "Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds."//0//1658bp//98%//AF089816

C-NT2RM2002145// "Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."//8.5E-191//1524bp//81%//AF084928

C-NT2RM4000027

C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146

C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003

C-NT2RM4000155// "THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS)."//1.2E-157//321aa//61%//P26639

C-NT2RM4000156//H.sapiens HPBR11-7 gene.//3.6E-21//785bp//60%//X67336

C-NT2RM4000167// "Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds."//0//1946bp//99%//AF071592

C-NT2RM4000199

C-NT2RM4000200

C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%/Q16600

C-NT2RM4000233// "Mus musculus semaphorin VIa mRNA, complete cds."//3.4E-231//1395bp//86%//AF030430

C-NT2RM4000244

C-NT2RM4000251

C-NT2RM4000265

C-NT2RM4000324

C-NT2RM4000327

C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292

C-NT2RM4000425

C-NT2RM4000433// "Mus musculus retinoic acid-responsive protein (Stra6) m

RNA, complete cds."//4.1E-271//2085bp//77%//AF062476

C-NT2RM4000514

C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//Q07230

C-NT2RM4000532

C-NT2RM4000534

C-NT2RM4000603

C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808

C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.7E-146//420aa//60%//P27550

C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P74168

C-NT2RM4000689

C-NT2RM4000698

C-NT2RM4000700

C-NT2RM4000712// "Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds."//1E-136//1104bp//77%//AF022789

C-NT2RM4000717

C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154

C-NT2RM4000734// "Homo sapiens mRNA for KIAA0760 protein, partial cds."//0//2273bp//99%//AB018303

C-NT2RM4000741// "Homo sapiens hSGT1 mRNA for hSgt1p, complete cds."//0//2184bp//99%//D88208

C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676

C-NT2RM4000764

C-NT2RM4000778

C-NT2RM4000787

C-NT2RM4000790

C-NT2RM4000795//”Homo sapiens mRNA for KIAA0951 protein, complete cds.”/  
/0//1847bp//96%//AB023168

C-NT2RM4000796

C-NT2RM4000798//”Homo sapiens brefeldin A-inhibited guanine nucleotide-e  
xchange protein 2 mRNA, complete cds.”//0//2603bp//99%//AF084521

C-NT2RM4000813

C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.3  
4) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682

C-NT2RM4000833

C-NT2RM4000848

C-NT2RM4000852

C-NT2RM4000855

C-NT2RM4000887

C-NT2RM4000895

C-NT2RM4000950

C-NT2RM4000979

C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp5  
86G0518).//0//2259bp//100%//AL050092

C-NT2RM4001032

C-NT2RM4001047//M025 PROTEIN.//8E-140//333aa//80%//Q06138

C-NT2RM4001054//”Homo sapiens sec61 homolog mRNA, complete cds.”//3.1E-1  
90//1315bp//81%//AF077032

C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.  
//0.000000032//165aa//33%//Q09820

C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II./  
/5.9E-86//292aa//48%//Q09417

C-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//1E-11//103aa//38%//Q01704

C-NT2RM4001151

C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q2  
7969

C-NT2RM4001160

C-NT2RM4001187

C-NT2RM4001191// "Homo sapiens clone 24963 mRNA sequence, complete cds."//  
/0//1950bp//99%//AF131737

C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742

C-NT2RM4001203// "Homo sapiens mRNA for KIAA0839 protein, partial cds."//  
0//3047bp//99%//AB020646

C-NT2RM4001204// "Homo sapiens mRNA for KIAA1089 protein, partial cds."//  
0//2349bp//99%//AB029012

C-NT2RM4001217// "Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA,  
complete cds."//7.3E-148//1409bp//72%//AF059611

C-NT2RM4001256// "Xenopus laevis putative Zic3 binding protein mRNA, comp  
lete cds."//4.30E-55//289bp//77%//AF129131

C-NT2RM4001258

C-NT2RM4001309

C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137)  
(PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676

C-NT2RM4001316// "ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR  
(EC 1.3.99.3) (MCAD)."//2.3E-31//334aa//30%//P08503

C-NT2RM4001320// "Homo sapiens mRNA for Neuroblastoma, complete cds."//1.  
8E-39//728bp//64%//D89016

C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171  
aa//37%//P32626

C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC  
REGION.//8.1E-30//265aa//33%//P53742

C-NT2RM4001347// "Homo sapiens NY-REN-25 antigen mRNA, partial cds."//0//



2300bp//99%//AF155103

C-NT2RM4001371//”Homo sapiens IDN3 mRNA, partial cds.”//0//2524bp//99%//  
AB019494

C-NT2RM4001382//”Homo sapiens RanBP7/importin 7 mRNA, complete cds.”//2.  
2E-237//1079bp//99%//AF098799

C-NT2RM4001384

C-NT2RM4001410

C-NT2RM4001411//”Mus musculus Pro-rich, PH, SH2 domain-containing signal  
ing mediator (PSM) mRNA, complete cds.”//0//1962bp//87%//AF020526

C-NT2RM4001412//”Homo sapiens nGAP mRNA, complete cds.”//0//1918bp//99%/  
/AF047711

C-NT2RM4001414

C-NT2RM4001437

C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA  
LIGASE) (ILERS).//1.4E-118//444aa//46%//P73505

C-NT2RM4001454

C-NT2RM4001455

C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737

C-NT2RM4001489//”Homo sapiens mRNA for KIAA0685 protein, complete cds.”/  
/0//1810bp//99%//AB014585

C-NT2RM4001522

C-NT2RM4001557//”Homo sapiens mRNA for KIAA1040 protein, partial cds.”//  
0//1547bp//97%//AB028963

C-NT2RM4001565

C-NT2RM4001566//”Homo sapiens mRNA for KIAA1114 protein, complete cds.”/  
/0//1900bp//99%//AB029037

C-NT2RM4001582//”Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, com  
plete cds.”//1.5E-284//1082bp//90%//AF071317

C-NT2RM4001592//”Homo sapiens mRNA for KIAA1122 protein, partial cds.”//

0//2170bp//99%//AB032948

C-NT2RM4001594

C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750

C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203  
aa//39%//Q12600

C-NT2RM4001629//"MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LAR  
GE HOMOLOG 3)."//1.5E-93//278aa//38%//Q13368

C-NT2RM4001650

C-NT2RM4001662

C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REG  
ION.//2.7E-84//410aa//42%//P37339

C-NT2RM4001682

C-NT2RM4001710

C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q141  
41

C-NT2RM4001715

C-NT2RM4001731//"Homo sapiens mRNA for KIAA1004 protein, partial cds."//  
0//1922bp//100%//AB023221

C-NT2RM4001746

C-NT2RM4001754

C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-  
).//4.1E-186//639aa//58%//Q05512

C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q  
03164

C-NT2RM4001810//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//  
/0//2377bp//99%//AB020670

C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346

C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//32  
5aa//37%//P28160

C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%/P51523

C-NT2RM4001836

C-NT2RM4001841//”Homo sapiens mRNA for KIAA0920 protein, complete cds.”//0//1861bp//98%/AB023137

C-NT2RM4001842

C-NT2RM4001856

C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%/P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%/Y17711

C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//36%/Q15404

C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%/P47486

C-NT2RM4001922//”Homo sapiens mRNA for KIAA0957 protein, complete cds.”//0//2165bp//99%/AB023174

C-NT2RM4001930//”Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.”//0//1930bp//99%/AF102851

C-NT2RM4001940//”Homo sapiens timeless homolog mRNA, complete cds.”//0//2087bp//99%/AF098162

C-NT2RM4001953

C-NT2RM4001965

C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%/X99330

C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%/P51523

C-NT2RM4001984

C-NT2RM4001987//”NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSO

R (N-CAM 180) [CONTAINS: N-CAM 140].">//3.2E-17//281aa//30%/P16170  
 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 IN PMT6-PCT1 INTERGENIC REGION.//6.9E-94//589aa//35%/P42935  
 C-NT2RM4002018  
 C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.9E-53//1585bp/  
 /60%/AF104260  
 C-NT2RM4002044  
 C-NT2RM4002054  
 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, com  
 plete cds.//0//1865bp//99%/U82267  
 C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protei  
 n complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71%  
 //AF117755  
 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41  
 %//Q04652  
 C-NT2RM4002128  
 C-NT2RM4002140  
 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%/P24014  
 C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2  
 671bp//99%/AF084535  
 C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%/P21590  
 C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-A  
 LPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.2E-33//688aa  
 //27%/P08640  
 C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//  
 /3E-37//122aa//72%/Q07803  
 C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-  
 1) mRNA, complete cds.//0//2452bp//100%/AF157028  
 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%/

P40809

C-NT2RM4002251//”ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCO  
SAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROT  
EIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).”//2.2E-36/  
/320aa//38%//P27808

C-NT2RM4002256

C-NT2RM4002266

C-NT2RM4002281

C-NT2RM4002287

C-NT2RM4002294

C-NT2RM4002301

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778

C-NT2RM4002339

C-NT2RM4002344

C-NT2RM4002373//”Homo sapiens mRNA for KIAA0649 protein, complete cds.”/  
/0//2666bp//99%//AB014549

C-NT2RM4002374

C-NT2RM4002383

C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA  
LIGASE) (ACYL- ACTIVATING ENZYME).//1.3E-29//275aa//30%//P27095

C-NT2RM4002438//”Xenopus laevis putative Zic3 binding protein mRNA, comp  
lete cds.”//1.1E-49//611bp//70%//AF129131

C-NT2RM4002446

C-NT2RM4002452

C-NT2RM4002457

C-NT2RM4002460//”ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROT  
EINS GP70, GP20].”//0.0000016//226aa//24%//P51515

C-NT2RM4002493

C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//3

66aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137

C-NT2RM4002558//”Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.”//0//1797bp//99%//AF055899

C-NT2RM4002567

C-NT2RM4002593

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%//032038

C-NT2RP1000324

C-NT2RP1000363//”Homo sapiens mRNA for KIAA0638 protein, partial cds.”//0//1345bp//99%//AB014538

C-NT2RP1000418

C-NT2RP1000513//”Human NifU-like protein (hNifU) mRNA, partial cds.”//6.50E-171//516bp//99%//U47101

C-NT2RP1000721

C-NT2RP1000730

C-NT2RP1000767

C-NT2RP1000836

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//33%//Q09531

C-NT2RP1000943

C-NT2RP1001033//”Homo sapiens delta-tubulin mRNA, complete cds.”//2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//”Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.”//8.1E-107//504bp//99%//AF182291

C-NT2RP1001199

C-NT2RP1001248

C-NT2RP1001253//”Homo sapiens oscillin (hLn) mRNA, complete cds.”//0//20

20bp//99%//AF029914

C-NT2RP1001286

C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//3  
2%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//3  
2%//Q12024

C-NT2RP1001310//”Homo sapiens mitochondrial carrier homolog 1 isoform a  
mRNA, partial cds; nuclear gene for mitochondrial product.”//0//1732bp//  
99%//AF176006

C-NT2RP1001361//”Homo sapiens NADH-ubiquinone oxidoreductase subunit B14  
.5B homolog mRNA, complete cds.”//6.5E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC RE  
GION.//2.7E-22//284aa//25%//P40074

C-NT2RP1001432

C-NT2RP2000040//”Homo sapiens mRNA for KIAA0747 protein, partial cds.”//  
0//2648bp//99%//AB018290

C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH  
2 gene).//7.9E-20//265bp//73%//AJ242730

C-NT2RP2000098

C-NT2RP2000108

C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa/  
/36%//P40556

C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE S  
UBUNIT) (A1 140 KD SUBUNIT) (RF-C. 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUB  
UNIT) (DNA-BINDING PROTEIN PO-GA).//7.1E-12//213aa//23%//P35251

C-NT2RP2000289

C-NT2RP2000327

C-NT2RP2000337

C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910

C-NT2RP2000459  
C-NT2RP2000498  
C-NT2RP2000758  
C-NT2RP2001137  
C-NT2RP2001149  
C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%/P37370  
C-NT2RP2001173//”Homo sapiens mRNA for KIAA0480 protein, complete cds.”/  
/0//1780bp//99%/AB007949  
C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-1  
0//88aa//38%/P18722  
C-NT2RP2001196  
C-NT2RP2001226  
C-NT2RP2001268//”Homo sapiens mRNA for KIAA0810 protein, partial cds.”//  
0//3301bp//98%/AB018353  
C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-AL  
PHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//4.4E-91//179aa//99%/P2866  
3  
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%/P  
20107  
C-NT2RP2001312  
C-NT2RP2001327//”TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHE  
LIAL (B12 PROTEIN).”//5.5E-116//311aa//71%/Q13829  
C-NT2RP2001328  
C-NT2RP2001366  
C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//2  
5%/Q02817  
C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.2  
1.-).//8.4E-192//581aa//54%/P93647  
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%/Y1



8004

C-NT2RP2001420// "Mus musculus nuclear protein NIP45 mRNA, complete cds."  
//9E-112//742bp//82%//U76759

C-NT2RP2001450

C-NT2RP2001467

C-NT2RP2001506

C-NT2RP2001511// "Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//3.2E-297//2206bp//75%//AF093097

C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL  
AR1.//0//2502bp//99%//Y14494

C-NT2RP2001536// "Homo sapiens X-ray repair cross-complementing protein 3  
(XRCC3) mRNA, complete cds."//0//2326bp//99%//AF035586

C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992

C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//  
8.2E-29//294aa//31%//Q09837

C-NT2RP2001581

C-NT2RP2001597// "RYANODINE RECEPTOR, CARDIAC MUSCLE."//0.000000036//127a  
a//36%//P30957

C-NT2RP2001628

C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (  
2-PHOSPHO-D- GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%//P4  
2897

C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS)  
(FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1  
) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//  
97%//P14324

C-NT2RP2001813

C-NT2RP2001883// "Homo sapiens CGI-01 protein mRNA, complete cds."//0//23  
06bp//99%//AF132936

C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%/P53946  
 C-NT2RP2001947  
 C-NT2RP2001985//”Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.”//2.00E-38//435bp//67%/AF090989  
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%/Q08469  
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.7E-47//247aa//52%/P35331  
 C-NT2RP2002058//”Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.”//0//2510bp//99%/AF083217  
 C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.5E-294//1334bp//99%/AF052183  
 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%/P18490  
 C-NT2RP2002079//”HISTONE H1, GONADAL.”//4.4E-11//214aa//34%/P02256  
 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%/AJ007509  
 C-NT2RP2002185//”Homo sapiens ubiquilin mRNA, complete cds.”//0//1789bp//99%/AF176069  
 C-NT2RP2002193//”Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.”//0//2809bp//99%/AB021868  
 C-NT2RP2002231  
 C-NT2RP2002235  
 C-NT2RP2002252//”Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.”//0//3118bp//91%/L38621  
 C-NT2RP2002292  
 C-NT2RP2002408  
 C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%/P46037  
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171a

a//27%//P30620

C-NT2RP2002498

C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%/  
/Q02386

C-NT2RP2002520//”Homo sapiens transcription factor RFX-B (RFXB) mRNA, co  
mplete cds.”//3.70E-34//668bp//61%//AF105427

C-NT2RP2002549

C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HM  
SH).//2.80E-08//109aa//37%//P19076

C-NT2RP2002706

C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%//P55194

C-NT2RP2002800

C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//2  
3%//P14922

C-NT2RP2002891

C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN  
D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%//Q18964

C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%//P52737

C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7  
.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700

C-NT2RP2003034

C-NT2RP2003099

C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117

C-NT2RP2003157//”Homo sapiens CGI-74 protein mRNA, complete cds.”//0//20  
37bp//99%//AF151832

C-NT2RP2003158//”Homo sapiens mRNA for proteasome subunit p58, complete  
cds.”//0//2091bp//99%//D67025

C-NT2RP2003165

C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein whic

h interacts with transcription factor Spl.//0//1544bp//99%/AJ242978  
 C-NT2RP2003277//”Homo sapiens mRNA for KIAA0625 protein, partial cds.”//  
 0//3788bp//99%/AB014525  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4)  
 (RNA-3' - PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%/Q23400  
 C-NT2RP2003297  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%/Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%/P17886  
 C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.  
 000022//261aa//24%/P48754  
 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//15  
 09bp//99%/AJ133769  
 C-NT2RP2003393  
 C-NT2RP2003445  
 C-NT2RP2003466//”Homo sapiens delta-6 fatty acid desaturase mRNA, comple  
 te cds.”//0//2194bp//99%/AF126799  
 C-NT2RP2003480//”Homo sapiens zinc finger DNA binding protein 99 (ZNF281  
 ) mRNA, complete cds.”//0//3012bp//99%/AF125158  
 C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4  
 E-14//106aa//46%/P04175  
 C-NT2RP2003511  
 C-NT2RP2003513//”Human mRNA for KIAA0270 gene, partial cds.”//0//2137bp/  
 /97%/D87460  
 C-NT2RP2003567//”Homo sapiens mRNA for KIAA0462 protein, partial cds.”//  
 0//2343bp//99%/AB007931  
 C-NT2RP2003604//”Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA,  
 complete cds.”//0//2442bp//99%/AF030233  
 C-NT2RP2003691  
 C-NT2RP2003713//”Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA,

complete cds."//0//2018bp//99%//AF073344  
 C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).  
 //0//869aa//80%//P53620  
 C-NT2RP2003764  
 C-NT2RP2003769  
 C-NT2RP2003777  
 C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3  
 .7E-21//137aa//43%//Q11076  
 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION P  
 ROTEIN).//0.00000016//117aa//29%//Q91955  
 C-NT2RP2003981//"Homo sapiens mRNA for KIAA0804 protein, partial cds."//  
 0//3046bp//99%//AB018347  
 C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp56  
 4A026).//0//2514bp//99%//AL050367  
 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599  
 C-NT2RP2004066//"Human DNA sequence from clone 134019 on chromosome 1p36  
 .11-36.33, complete sequence."//0//2410bp//99%//AL034555  
 C-NT2RP2004081  
 C-NT2RP2004124  
 C-NT2RP2004152  
 C-NT2RP2004165  
 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION  
 FACTOR RU49).//5.6E-31//424aa//28%//Q07231  
 C-NT2RP2004239//"Homo sapiens lok mRNA for protein kinase, complete cds.  
 " //0//3044bp//99%//AB015718  
 C-NT2RP2004245  
 C-NT2RP2004364  
 C-NT2RP2004365  
 C-NT2RP2004366//"Homo sapiens mRNA for KIAA0986 protein, partial cds."//

0//2790bp//97%//AB023203

C-NT2RP2004373

C-NT2RP2004476// "Homo sapiens cyclin L ania-6a mRNA, complete cds."//0//

2075bp//99%//AF180920

C-NT2RP2004551

C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//

625aa//40%//Q09903

C-NT2RP2004600

C-NT2RP2004664// "Homo sapiens mRNA for KIAA0460 protein, partial cds."//

0//2368bp//99%//AB007929

C-NT2RP2004743

C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RIC

H KINASE 1).//1.3E-26//190aa//41%//P38692

C-NT2RP2004816// "Homo sapiens H beta 58 homolog mRNA, complete cds."//0//

/2144bp//96%//AF054179

C-NT2RP2004861

C-NT2RP2004897

C-NT2RP2004933// "Homo sapiens mRNA for ZIP-kinase, complete cds."//0//21

03bp//99%//AB007144

C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386

C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL AD

DITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFER

ASE).//4E-91//218aa//44%//Q92089

C-NT2RP2005162// "Homo sapiens aspartyl aminopeptidase mRNA, complete cds

."//0//1615bp//99%//AF005050

C-NT2RP2005204// "Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA

1) mRNA, complete cds."//0//1262bp//99%//AF090385

C-NT2RP2005227

C-NT2RP2005287

C-NT2RP2005288//”Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.”//0//2992bp//99%//AF060219

C-NT2RP2005490//”Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.”//1.8E-175//1102bp//83%//AF053628

C-NT2RP2005539//”Homo sapiens mRNA for KIAA0850 protein, complete cds.”//0//1560bp//99%//AB020657

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053

C-NT2RP2005722//”Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.”//0//2545bp//99%//AB011414

C-NT2RP2005732

C-NT2RP2005784//”Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.”//0//2191bp//92%//AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//318aa//31%//P40004

C-NT2RP2005859//”Homo sapiens mRNA for KIAA0863 protein, complete cds.”//0//1649bp//99%//AB020670

C-NT2RP2006023

C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//AL080155

C-NT2RP2006441

C-NT2RP3000002

C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//53%//Q05481

C-NT2RP3000055

C-NT2RP3000068

C-NT2RP3000080

C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CO

NTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)] ./1.9E-123//436aa//50%/P46401

C-NT2RP3000092

C-NT2RP3000109//P54 PROTEIN PRECURSOR./0.0000065//358aa//22%/P13692

C-NT2RP3000134

C-NT2RP3000149

C-NT2RP3000197

C-NT2RP3000207//”GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).”//2.9E-11//721aa //23%/P08640

C-NT2RP3000233//”Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins. Contains ESTs and GSSs, complete sequence.”//0//1462bp//99%/AL035424

C-NT2RP3000235

C-NT2RP3000247

C-NT2RP3000267

C-NT2RP3000299//”Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.”//0//2730bp//82%/D29766

C-NT2RP3000324

C-NT2RP3000341//”Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.”//1.5E-246//1124bp//99%/AF106622

C-NT2RP3000393//”Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.”//5.8E-266//1373bp//86%/AF061817

C-NT2RP3000441//”Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.”//3.40E-42//645bp//67%/AF098066

C-NT2RP3000449

C-NT2RP3000451



C-NT2RP3000456  
C-NT2RP3000542  
C-NT2RP3000561  
C-NT2RP3000562//”Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.”//0//2165bp//99%//AF093097  
C-NT2RP3000578//HES1 PROTEIN.//1.3E-22//229aa//27%//P35843  
C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288  
C-NT2RP3000592  
C-NT2RP3000622  
C-NT2RP3000624  
C-NT2RP3000685  
C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//Q14153  
C-NT2RP3000742//”1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-II I) (FRAGMENT).”//4.1E-165//371aa//49%//P10895  
C-NT2RP3000753  
C-NT2RP3000826  
C-NT2RP3000865  
C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426  
C-NT2RP3001007  
C-NT2RP3001055  
C-NT2RP3001111//”Homo sapiens TRF-proximal protein mRNA, complete cds.”//1.50E-149//731bp//97%//AF097725  
C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737  
C-NT2RP3001126  
C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154

C-NT2RP3001232

C-NT2RP3001268//”Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.”//0//3606bp//99%//AF198358

C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.3E-99//669bp//83%//Y18101

C-NT2RP3001274//”Homo sapiens mRNA for KIAA1037 protein, partial cds.”//0//2254bp//99%//AB028960

C-NT2RP3001281

C-NT2RP3001297

C-NT2RP3001318

C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%/P51508

C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%/P32089

C-NT2RP3001374

C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%/P12270

C-NT2RP3001432

C-NT2RP3001447

C-NT2RP3001449//”Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG

islands, ESTs, STSs and GSSs, complete sequence."//0//1827bp//99%/AL03  
1282

C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY  
ANTIGEN MODIFIER 2).//3.2E-90//157aa//59%/P36371

C-NT2RP3001459

C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds."//4.3E-  
290//793bp//93%/U63420

C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//  
9.10E-10//158aa//31%/Q10022

C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl  
) mRNA, complete cds."//0//1730bp//85%/AF163665

C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, com  
plete cds."//0//2617bp//99%/U35832

C-NT2RP3001589

C-NT2RP3001607

C-NT2RP3001608

C-NT2RP3001671//Homo sapiens mRNA for KIAA0850 protein, complete cds."/  
/0//2310bp//99%/AB020657

C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SC  
MH1) mRNA, complete cds."//0//2836bp//99%/AF149046

C-NT2RP3001678

C-NT2RP3001688//Homo sapiens glucocorticoid modulatory element binding  
protein-1 (GMEB1) mRNA, complete cds."//0//1695bp//99%/AF099013

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0000002  
4//481aa//21%/P25386

C-NT2RP3001698

C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa/  
/32%/P54356

C-NT2RP3001716

C-NT2RP3001752

C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.  
8E-117//462aa//55%//P52272

C-NT2RP3001844

C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp56  
4G013).//0//1528bp//99%//AL050011

C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.1E  
-125//302aa//60%//P55347

C-NT2RP3001898//”Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,  
3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.  
”//0//1587bp//100%//AB000624

C-NT2RP3001931

C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%//P37709

C-NT2RP3002002

C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%//  
X86779

C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%//P39955

C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III./  
/5.30E-25//139aa//48%//Q09232

C-NT2RP3002045//”Homo sapiens mRNA for KIAA0899 protein, partial cds.”//  
0//3385bp//99%//AB020706

C-NT2RP3002056//”Homo sapiens Rb binding protein homolog mRNA, partial c  
ds.”//0//2374bp//99%//AF083249

C-NT2RP3002062//”Homo sapiens mRNA for KIAA0873 protein, partial cds.”//  
0//3764bp//99%//AB020680

C-NT2RP3002081//”Xenopus laevis chromosome condensation protein XCAP-G m  
RNA, complete cds.”//4.1E-233//1896bp//69%//AF111423

C-NT2RP3002097

C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12

387

C-NT2RP3002142

C-NT2RP3002146

C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING  
PROTEIN GST1-HS).//2.8E-253//474aa//93%/P15170

C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.9E-151//223a  
a//91%/Q02614

C-NT2RP3002166

C-NT2RP3002181

C-NT2RP3002244

C-NT2RP3002248

C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%/P45978

C-NT2RP3002276

C-NT2RP3002304

C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE  
DEAMINASE).//3.70E-43//318aa//37%/P05792

C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting  
.//0//2276bp//99%/AJ133421

C-NT2RP3002566

C-NT2RP3002587

C-NT2RP3002590

C-NT2RP3002631

C-NT2RP3002650//”Mus musculus growth suppressor 1L (Gros1) mRNA, complet  
e cds.”//0//2109bp//87%/AF165163

C-NT2RP3002663//”Homo sapiens putative glycolipid transfer protein mRNA,  
complete cds.”//8.10E-263//1243bp//97%/AF103731

C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%/P1306

0

C-NT2RP3002763

C-NT2RP3002861

C-NT2RP3002911

C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%/Q04652

C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds."//0//2388bp//99%//AF152498

C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds."//1.8E-292//1325bp//99%//AF080158

C-NT2RP3003008

C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds."//3.6E-83//807bp//72%//D88315

C-NT2RP3003204

C-NT2RP3003278

C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds."//0//2596bp//98%//L36983

C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds."//1.5e-310//1468bp//82%//AB033922

C-NT2RP3003302

C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds."//0//2476bp//99%//AF117657

C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.3E-35//178aa//44%//Q62191

C-NT2RP3003344

C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084

C-NT2RP3003377

C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds."//0//2133bp//85%/U09874

C-NT2RP3003433

C-NT2RP3003490// "Homo sapiens mRNA for KIAA0725 protein, partial cds."//  
0//2437bp//99%//AB018268

C-NT2RP3003491// "Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds."//5.6E-36//842bp//62%//AF091624

C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886

C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820

C-NT2RP3004209// "Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds."//0//2320bp//99%//AF126736

C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%  
//P52734

C-NT2RP3004246

C-NT2RP3004258// "Homo sapiens ZIS1 mRNA, complete cds."//0//1861bp//99%  
/AF065391

C-NT2RP3004262// "Homo sapiens heat shock protein hsp40-3 mRNA, complete cds."//2.4E-248//1126bp//100%//AF088982

C-NT2RP3004341

C-NT2RP3004378

C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%//AJ007798

C-NT2RP3004428

C-NT2RP3004451

C-NT2RP3004454// "Homo sapiens mRNA for KIAA0448 protein, complete cds."//  
/0//2875bp//99%//AB007917

C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%//Q01820

C-NT2RP3004498// "Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds."//2E-249//1777bp//80%//U83176

C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%/Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%/P40484

C-NT2RP3004534//"Mouse oncogene (ect2) mRNA, complete cds."//0//2075bp//87%/L11316

C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%/P33755

C-NT2RP4000907//"Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds."//0//2127bp//86%/D45913

C-NT2RP4001029//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//0//1711bp//90%/U20086

C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//186aa//29%/O24076

C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%/P35844

C-NT2RP4001442

C-NT2RP4001529//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//1.70E-255//1148bp//90%/U20086

C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%/P12868

C-OVARC1000106//"TROPOMYOSIN 1, FUSION PROTEIN 33."//0.000032//165aa//27%/P49455

C-OVARC1000198

C-OVARC1000682//"PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)."//1.1E-209//293aa//95%/P39098

C-OVARC1000703

C-OVARC1000722//"Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds."//0//759bp//98%/AF038661

C-OVARC1000730

C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%



//P25159

C-OVARC1000781

C-OVARC1000787

C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2  
.8E-258//1183bp//99%//Y17711

C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199

C-OVARC1000850//”Homo sapiens PB39 mRNA, complete cds.”//0//2095bp//99%/  
/AF045584

C-OVARC1000862//M.musculus mRNA for FT1.//5.9E-226//1498bp//81%//Z67963

C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%//P404  
84

C-OVARC1000883

C-OVARC1000886

C-OVARC1000912

C-OVARC1000915//”Homo sapiens histone deacetylase 5 mRNA, complete cds.”  
//1.60E-121//591bp//97%//AF132608

C-OVARC1000924

C-OVARC1000964

C-OVARC1000984

C-OVARC1001004

C-OVARC1001010

C-OVARC1001011

C-OVARC1001032

C-OVARC1001044

C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//9  
8%//P43490

C-OVARC1001068//”Homo sapiens Era GTPase A protein (HERA-A) mRNA, partia  
l cds.”//0//1819bp//99%//AF082657

C-OVARC1001074

C-OVARC1001092//”Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).”//2E-214//769bp//97%//AJ005897

C-OVARC1001107//”Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.”//6.1E-276//594bp//98%//AF167572

C-OVARC1001154//”Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.”//2.3E-296//1561bp//93%//AF055008

C-OVARC1001161

C-OVARC1001167

C-OVARC1001170

C-OVARC1001171//”Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.”//5.7E-151//436bp//92%//U94855

C-OVARC1001173

C-OVARC1001176

C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510

C-OVARC1001188

C-OVARC1001232//”CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).”//5.10E-22//83aa//37%//Q10568

C-OVARC1001270

C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%//P25976

C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444

C-OVARC1001344

C-OVARC1001369

C-OVARC1001372//”Homo sapiens mRNA for KIAA0897 protein, partial cds.”//0//840bp//97%//AB020704

C-OVARC1001391

C-OVARC1001399

C-OVARC1001417//”Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds.”//0//1715bp//99%//AF135802

C-OVARC1001419//”Homo sapiens GOK (STIM1) mRNA, complete cds.”//4.9E-48//586bp//69%//U52426

C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111

C-OVARC1001453

C-OVARC1001476//”Mus musculus YGR163w mRNA homologue, complete cds.”//1.80E-187//510bp//89%//AB017616

C-OVARC1001480

C-OVARC1001489

C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161

C-OVARC1001525

C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081

C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retroseudogene.//0//1167bp//100%//AF031165

C-OVARC1001600

C-OVARC1001610//”Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.”//0//1870bp//99%//AF068302

C-OVARC1001702

C-OVARC1001703//”Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.”//3.5E-16//399bp//61%//AF133670

C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1B).//2.80E-10//106aa//38%//Q62267

C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106

C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%

//Q13796

C-OVARC1001731//”TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.”//4E-12  
2//282aa//85%//P08942

C-OVARC1001745

C-OVARC1001762//”N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TER  
MINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).”//6.4E-85//514aa//34%//P12945

C-OVARC1001766//”Homo sapiens eukaryotic translation initiation factor e  
IF3, p35 subunit mRNA, complete cds.”//0//963bp//99%//U97670

C-OVARC1001767//”Homo sapiens mRNA for KIAA0675 protein, complete cds.”/  
/0//2083bp//99%//AB014575

C-OVARC1001768

C-OVARC1001791

C-OVARC1001795

C-OVARC1001802

C-OVARC1001809//”Mus musculus sphingosine kinase (SPHK1a) mRNA, partial  
cds.”//2.7E-190//1624bp//76%//AF068748

C-OVARC1001828

C-OVARC1001846

C-OVARC1001861

C-OVARC1001879

C-OVARC1001880

C-OVARC1001883

C-OVARC1001916

C-OVARC1001928

C-OVARC1001942//”N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TER  
MINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).”//3.1E-81//497aa//35%//P12945

C-OVARC1001943//”Mus musculus DEBT-91 mRNA, complete cds.”//0//2035bp//8  
7%//AF143859

C-OVARC1001950

C-OVARC1001987//”Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.”//2.3E-220//652bp//84%//AF061817

C-OVARC1002050//”Homo sapiens mRNA for actin binding protein ABP620, complete cds.”//0//1019bp//99%//AB029290

C-OVARC1002082

C-OVARC1002107

C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//035913

C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955

C-OVARC1002156

C-OVARC1002158

C-PLACE1000004//”Homo sapiens IDN3-B mRNA, complete cds.”//0//2365bp//99%//AB019602

C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%/P08643

C-PLACE1000048

C-PLACE1000050

C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154

C-PLACE1000081//”Human SEC7 homolog Tic (TIC) mRNA, complete cds.”//0//2077bp//99%//U63127

C-PLACE1000094

C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8E-62//158aa//81%//P20290

C-PLACE1000214

C-PLACE1000236

C-PLACE1000246

C-PLACE1000292

C-PLACE1000308

C-PLACE1000332

C-PLACE1000453

C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60  
E-47//207aa//46%/P51522

C-PLACE1000599

C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%/P52918

C-PLACE1000653// "Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,  
complete cds."//0//1992bp//99%/AF180371

C-PLACE1000656// "Homo sapiens mRNA for JM4 protein, complete CDS (clone  
IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))."//2.1E-277//1260bp//99%  
//AJ005896

C-PLACE1000706// "Homo sapiens transcriptional intermediary factor 1 gamm  
a mRNA, complete cds."//0//1366bp//99%/AF119043

C-PLACE1000712

C-PLACE1000749

C-PLACE1000769// "Homo sapiens CGI-18 protein mRNA, complete cds."//0//19  
85bp//98%/AF132952

C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO  
/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%  
//P52734

C-PLACE1000849

C-PLACE1000856// "Homo sapiens mRNA for KIAA0974 protein, partial cds."//  
0//1310bp//100%/AB023191

C-PLACE1000931

C-PLACE1000987// "Homo sapiens mRNA for KIAA0724 protein, complete cds."/  
/0//1749bp//99%/AB018267

C-PLACE1001010

C-PLACE1001015

C-PLACE1001024

C-PLACE1001062// "Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence."//2.7E-32//470bp//71%//AC006020

C-PLACE1001104

C-PLACE1001168

C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496

C-PLACE1001185// "Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//1668bp//99%//AB023160

C-PLACE1001238// "Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//2E-202//1333bp//80%//D14336

C-PLACE1001280

C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X71642

C-PLACE1001304// "Homo sapiens zinc finger protein dp mRNA, complete cds."//0//2421bp//99%//AF153201

C-PLACE1001311

C-PLACE1001323

C-PLACE1001351

C-PLACE1001414

C-PLACE1001440

C-PLACE1001456

C-PLACE1001517// "Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds."//4.60E-112//392bp//87%//AB002137

C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809

C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//P51523

C-PLACE1001634

C-PLACE1001640

C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-6

6//174aa//45%//P91408  
C-PLACE1001705  
C-PLACE1001716  
C-PLACE1001720  
C-PLACE1001745  
C-PLACE1001748//”Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds  
.”//0//2602bp//99%//AF061243  
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential prote  
in TRP6.//0//2900bp//99%//AJ006276  
C-PLACE1001799  
C-PLACE1001845//”Mus musculus cyclin ania-6a mRNA, complete cds.”//3.30E  
-31//925bp//62%//AF159159  
C-PLACE1001897  
C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E  
-58//112aa//100%//076094  
C-PLACE1002157  
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX C  
OMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591  
C-PLACE1002227  
C-PLACE1002259  
C-PLACE1002319  
C-PLACE1002395//”Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, comple  
te cds.”//7.9E-100//966bp//75%//AB030505  
C-PLACE1002477  
C-PLACE1002493//”Homo sapiens signal transducing adaptor molecule 2A (ST  
AM2) mRNA, complete cds.”//1.7E-113//545bp//98%//AF042273  
C-PLACE1002500  
C-PLACE1002514  
C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396



C-PLACE1002537

C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%/P45890

C-PLACE1002583//”GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).”//5.6E-34//76aa//98%/P39087

C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%/P45340

C-PLACE1002625

C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.5E-278//543aa//92%/Q28046

C-PLACE1002768

C-PLACE1002782//”Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.”//3.8E-43//385bp//77%/U50927

C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%/P53973

C-PLACE1002853

C-PLACE1002908//”Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.”//0//1654bp//99%/AB028600

C-PLACE1002962

C-PLACE1002968

C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%/Q49091

C-PLACE1003025

C-PLACE1003027//”Homo sapiens mRNA for KIAA0516 protein, partial cds.”//2.1e-314//1417bp//100%/AB011088

C-PLACE1003044//”Homo sapiens mRNA for KIAA0829 protein, partial cds.”//0//1382bp//96%/AB020636

C-PLACE1003176

C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%/Q15391

C-PLACE1003256

C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa//47%/  
/P21541

C-PLACE1003343

C-PLACE1003361

C-PLACE1003366//”Homo sapiens otoferlin (OTOF) mRNA, complete cds.”//1.4  
E-78//542bp//67%//AF107403

C-PLACE1003373

C-PLACE1003375

C-PLACE1003394//”Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.”  
//2.30E-150//774bp//94%//M83680

C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W://1.3E-40//278aa/  
/36%//P40556

C-PLACE1003454

C-PLACE1003478

C-PLACE1003516

C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136

C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000  
011//101aa//32%//Q09475

C-PLACE1003528

C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PRO  
TEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC  
INTERMEDIATE COMPONENT).//7.7E-68//404aa//33%//P32802

C-PLACE1003566

C-PLACE1003584

C-PLACE1003593

C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.00000023//82aa//35%//  
Q02516

C-PLACE1003618

C-PLACE1003638

C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%/P52742

C-PLACE1003760//”Homo sapiens tetraspanin TM4-A mRNA, complete cds.”//5.

2E-289//1313bp//97%/AF133423

C-PLACE1003768

C-PLACE1003795

C-PLACE1003886

C-PLACE1003888//”Homo sapiens mRNA for KIAA1092 protein, partial cds.”//

0//2057bp//99%/AB029015

C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//584aa//74%/P17812

C-PLACE1003915//”PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGASE) (ARGRS).”//2.4E-108//581aa//40%/Q05506

C-PLACE1004118

C-PLACE1004256//”Mus musculus short coiled coil protein SCOCO (Scoc) mRNA A, complete cds.”//2E-93//960bp//76%/AF115778

C-PLACE1004274

C-PLACE1004284

C-PLACE1005331

C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//99%/AL050267

C-PLACE1005828

C-PLACE1005876//”CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).”//0//730aa//99%/Q10568

C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%/P54069

C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//30%/P98110

C-PLACE1007053

C-PLACE1007068

C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%  
//Q04652

C-PLACE1009921

C-PLACE1010401

C-PLACE1010856

C-PLACE1010857

C-PLACE1010917

C-PLACE1010925

C-PLACE1010926//”Homo sapiens mRNA for KIAA0554 protein, partial cds.”//  
0//1160bp//100%//AB011126

C-PLACE1010942//”Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.”//0//1440bp//99%//AF114487

C-PLACE1010944

C-PLACE1010954

C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890

C-PLACE1011026

C-PLACE1011046//”1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).”//0//646aa//97%//P10894

C-PLACE1011054

C-PLACE1011057

C-PLACE1011109//”ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).”//  
/1.50E-22//63aa//88%//Q07803

C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532

C-PLACE1011133

C-PLACE1011143

C-PLACE1011165

C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100  
%/P03830

C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.).//3.2E-12//212aa//2  
9%/Q03326

C-PLACE1011221

C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp56  
40043).//0//2487bp//99%/AL050390

C-PLACE1011325

C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,  
complete cds.//7.2E-151//697bp//99%/AF102265

C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380  
bp//97%/AB019602

C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.2E-  
90//427bp//99%/AF151830

C-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//  
0//1946bp//99%/AB011102

C-PLACE1011452

C-PLACE1011465

C-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//  
/0//2022bp//99%/AB018255

C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.  
//0//2040bp//99%/AF065482

C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSO  
R (CTPT).//4.90E-11//147aa//32%/P52178

C-PLACE1011520

C-PLACE1011563

C-PLACE1011567

C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA,  
complete cds.//0//1791bp//82%/L11672

C-PLACE1011586  
C-PLACE1011643  
C-PLACE1011649  
C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%/P17886  
C-PLACE1011682  
C-PLACE1011719  
C-PLACE1011729  
C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp//99%/AL050287  
C-PLACE1011874  
C-PLACE1011875//"Homo sapiens mRNA for KIAA0580 protein, partial cds."//4.1E-112//524bp//100%/AB011152  
C-PLACE1011923//"Homo sapiens serum-inducible kinase mRNA, complete cds."//0//2782bp//99%/AF059617  
C-PLACE1011982  
C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%/Q09475  
C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%/P42566  
C-PLACE2000017  
C-PLACE2000021//"Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds."//2.7E-107//981bp//74%/AF082556  
C-PLACE2000047  
C-PLACE2000062//"Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347."//6.3E-166//656bp//94%/AB015629  
C-PLACE2000100  
C-PLACE2000111  
C-PLACE2000172

C-PLACE2000187

C-PLACE2000216// "Dog nonerythroid beta-spectrin mRNA, 3' end." //3.2E-253  
//1799bp//83%//L02897

C-PLACE2000246// "Homo sapiens mRNA for KIAA0795 protein, partial cds." //4.60E-172//796bp//99%//AB018338

C-PLACE2000317

C-PLACE2000341// "Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds." //0//1554bp//99%//AF069307

C-PLACE2000366

C-PLACE2000373// F-SPONDIN PRECURSOR. //8.6E-16//371aa//28%//P35446

C-PLACE2000394

C-PLACE2000398// LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48). //6.3E-37//90aa//98%//P10586

C-PLACE2000411// "Homo sapiens mRNA for KIAA1037 protein, partial cds." //0//2515bp//99%//AB028960

C-PLACE2000425

C-PLACE2000427// PROBABLE HELICASE MOT1. //1.2E-26//200aa//27%//P32333

C-PLACE2000433

C-PLACE2000438// "POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)." //2.1E-86//348aa//41%//Q10472

C-PLACE2000458// CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN). //2.5E-25//165aa//40%//P33450

C-PLACE2000477// "Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds." //6.7E-127//671bp//94%//AF072733

C-PLACE3000009

C-PLACE3000020// "Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds." //0//2253bp//99%//AF033861

C-PLACE3000103

C-PLACE3000142

C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205

C-PLACE3000156

C-PLACE3000157

C-PLACE3000197

C-PLACE3000208

C-PLACE3000226//”Homo sapiens mRNA for KIAA0962 protein, partial cds.”//  
0//4805bp//99%//AB023179

C-PLACE3000242//”Homo sapiens mRNA for KIAA1114 protein, complete cds.”/  
/0//2786bp//96%//AB029037

C-PLACE3000363

C-PLACE3000405

C-PLACE3000416//”Homo sapiens mRNA for actin binding protein ABP620, com  
plete cds.”//1.80E-141//565bp//98%//AB029290

C-PLACE3000477

C-PLACE4000106//”Homo sapiens mRNA for KIAA0462 protein, partial cds.”//  
0//6702bp//99%//AB007931

C-PLACE4000323

C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (U  
P-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771

C-PLACE4000369//”Homo sapiens mRNA for KIAA1025 protein, partial cds.”//  
0//4830bp//99%//AB028948

C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp43  
4C212).//0//2565bp//99%//AL080196

C-PLACE4000558//”Homo sapiens mRNA for KIAA0729 protein, partial cds.”//  
0//1051bp//97%//AB018272

C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED  
PROTEIN 1) (UEGF-1).//9.3E-70//226aa//52%//P10079



C-PLACE4000593

C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] .//7.1E-154//340aa//40%/P21414

C-PLACE4000670

C-THYRO1000026

C-THYRO1000085//”PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.”//2E-72//155aa//92%/Q06710

C-THYRO1000107

C-THYRO1000111.

C-THYRO1000132//”Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.”//1.1E-159//824bp//95%/U97018

C-THYRO1000156

C-THYRO1000173//”Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.”//0//1713bp//99%/AF020797

C-THYRO1000186

C-THYRO1000187

C-THYRO1000241

C-THYRO1000279

C-THYRO1000327//”Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.”//0//1567bp//99%/AF124145

C-THYRO1000452

C-THYRO1000471

C-THYRO1000484

C-THYRO1000502

C-THYRO1000505

C-THYRO1000585//”Homo sapiens protein associated with Myc mRNA, complete cds.”//0//1901bp//99%/AF075587

C-THYRO1000596

C-THYRO1000662// "Homo sapiens XPV mRNA for DNA polymerase eta, complete cds."//0//2341bp//99%//AB024313

C-THYRO1000666// Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889

C-THYRO1000715

C-THYRO1000734

C-THYRO1000748// RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171

C-THYRO1000756// "ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY)."//1.8E-55//243aa//42%//Q64686

C-THYRO1000777

C-THYRO1000783// "Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds."//2.4E-157//1656bp//70%//U37373

C-THYRO1000787

C-THYRO1000793

C-THYRO1000796

C-THYRO1000843

C-THYRO1000852// "Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds."//3.3E-147//790bp//93%//U68418

C-THYRO1000865

C-THYRO1000895

C-THYRO1000926// "Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds."//0//2387bp//99%//AF079529

C-THYRO1000951// DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%//P43550

C-THYRO1000952

C-THYRO1000983// UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.3

0E-17//143aa//39%/P35132

C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%/P52491

C-THYRO1001031

C-THYRO1001062

C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%/P98168

C-THYRO1001133

C-THYRO1001134// "Homo sapiens CGI-78 protein mRNA, complete cds."//0//1898bp//99%/AF151835

C-THYRO1001173

C-THYRO1001213

C-THYRO1001321

C-THYRO1001322

C-THYRO1001365

C-THYRO1001401

C-THYRO1001411

C-THYRO1001434

C-THYRO1001534

C-THYRO1001541

C-THYRO1001559

C-THYRO1001570

C-THYRO1001595

C-THYRO1001605

C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//99%/AJ002190

C-THYRO1001656// "Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-273//1947bp//82%/AF175968

C-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59  
kDa isoform.//0//1820bp//99%//AJ225089

C-THYR01001673

C-THYR01001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672

C-THYR01001706

C-THYR01001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//  
217aa//30%//P38584

C-THYR01001745

C-THYR01001793

C-THYR01001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P421  
28

C-THYR01001895

C-THYR01001907

C-VESEN1000122

C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916

C-Y79AA1000059// "Homo sapiens immunophilin homolog ARA9 mRNA, complete c  
ds."//2.9E-70//1040bp//65%//U78521

C-Y79AA1000065

C-Y79AA1000131

C-Y79AA1000181// "Homo sapiens CGI-01 protein mRNA, complete cds."//0//18  
58bp//99%//AF132936

C-Y79AA1000202

C-Y79AA1000214// "Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, compl  
ete cds."//7.1E-71//345bp//100%//AF081192

C-Y79AA1000230

C-Y79AA1000258

C-Y79AA1000268// "Mus musculus Nip2l mRNA, complete cds."//2.10E-50//648b  
p//64%//AF035207

C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910

C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25%//Q93794  
C-Y79AA1000355  
C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4E-20//2  
61aa//27%//P25343  
C-Y79AA1000420  
C-Y79AA1000469//”Mus musculus ancient ubiquitous 46 kDa protein AUP1 pre  
cursor (Aup1) mRNA, complete cds.”//8.30E-252//1207bp//85%//U41736  
C-Y79AA1000480  
C-Y79AA1000540  
C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALP  
HA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADA  
PTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//0//652aa//98%//P17427  
C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF  
103801  
C-Y79AA1000627//”Homo sapiens zinc finger protein (ZF5128) mRNA, complet  
e cds.”//2E-287//2031bp//82%//AF060503  
C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//14  
77bp//84%//X69942  
C-Y79AA1000734//”Homo sapiens peroxisomal biogenesis factor (PEX11b) mRN  
A, complete cds.”//0//1594bp//99%//AF093670  
C-Y79AA1000748//”Homo sapiens CGI-05 protein mRNA, complete cds.”//1.9E-  
239//1367bp//91%//AF152097  
C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRN  
P X) (CBP).//4.9E-91//200aa//64%//Q61990  
C-Y79AA1000774  
C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3E-37//4  
69aa//27%//P49902  
C-Y79AA1000784//”Homo sapiens RanBP7/importin 7 mRNA, complete cds.”//1.  
10E-236//1076bp//99%//AF098799

C-Y79AA1000794//”Homo sapiens actin-associated protein 2E4/kaplin (2E4)  
mRNA, 2E4-1 allele, complete cds.”//0//1610bp//99%//AF105369

C-Y79AA1000800//”Homo sapiens putative secreted protein (ZSIG11) mRNA, c  
omplete cds.”//1.6E-284//1288bp//99%//AF072733

C-Y79AA1000805

C-Y79AA1000824

C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//220aa//79%//P05209

C-Y79AA1000850

C-Y79AA1000962//”MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN  
II).”//4.2E-17//430aa//27%//Q99323

C-Y79AA1000968//”Rattus norvegicus initiation factor eIF-2B gamma subuni  
t (eIF-2B gamma) mRNA, complete cds.”//3.9E-248//1468bp//87%//U38253

C-Y79AA1000976

C-Y79AA1001023

C-Y79AA1001041

C-Y79AA1001048//”ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECUR  
SOR (EC 1.3.99.-) (VLCAD).”//3.1E-138//583aa//47%//P45953

C-Y79AA1001077

C-Y79AA1001078

C-Y79AA1001145

C-Y79AA1001177

C-Y79AA1001185

C-Y79AA1001211//”Homo sapiens origin recognition complex subunit 6 (ORC6  
) mRNA, complete cds.”//0//1435bp//99%//AF139658

C-Y79AA1001228

C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA  
-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa//42%//  
P51657

C-Y79AA1001236//”Homo sapiens mRNA for JM23 protein, complete coding seq

uence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))."//0//1653bp//99%//AJ005892

C-Y79AA1001281

C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.00000023//193aa//30%//Q03309

C-Y79AA1001323// "Mus musculus mRNA for GSG1, complete cds."//3.3E-172//1171bp//83%//D87325

C-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//1.2E-58//178aa//66%/P31271

C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa//32%//O83746

C-Y79AA1001402// "Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds."//8.50E-65//784bp//62%//AF083115

C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132

C-Y79AA1001533// "Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//4.5E-193//1333bp//80%//D14336

C-Y79AA1001541

C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.5E-76//85aa//90%//P42356

C-Y79AA1001555

C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.9E-40//482aa//27%//P27550

C-Y79AA1001585

C-Y79AA1001603// "POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."//1.7E-84//313aa//48%//Q07537

C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.8E-91//209aa//41%//P52740  
 C-Y79AA1001665  
 C-Y79AA1001679//”Homo sapiens lambda-crystallin mRNA, complete cds.”//3.4e-310//1430bp//98%//AF077049  
 C-Y79AA1001696//”Homo sapiens mRNA for KIAA1109 protein, partial cds.”//0//1669bp//100%//AB029032  
 C-Y79AA1001705//”Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.”//3.4E-47//626bp//68%//AF033120  
 C-Y79AA1001711//”Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.”//1.2E-258//1185bp//99%//J04137  
 C-Y79AA1001781  
 C-Y79AA1001805  
 C-Y79AA1001827//”Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.”//0//1689bp//98%//AF177145  
 C-Y79AA1001846  
 C-Y79AA1001923  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1E-10//94aa//47%//042643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743  
 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5E-163//752bp//99%//X86018  
 C-Y79AA1002089  
 C-Y79AA1002115  
 C-Y79AA1002125  
 C-Y79AA1002204  
 C-Y79AA1002208//ANKYRIN.//8.1E-34//188aa//38%//Q02357  
 C-Y79AA1002209//”Homo sapiens CGI-04 protein mRNA, complete cds.”//0//16



17bp//99%//AF132939

C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//7.10E-17//213a  
a//31%//P30620

C-Y79AA1002246//SYNAPTOTAGMIN V.//1.6E-28//286aa//32%//000445

C-Y79AA1002298

C-Y79AA1002307//”Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.”/  
/0//1209bp//99%//AF116574

C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding  
protein.//2.9E-186//1130bp//82%//X67877

C-Y79AA1002351

C-Y79AA1002407

C-Y79AA1002433//”Homo sapiens chromatin-specific transcription elongatio  
n factor FACT 140 kDa subunit mRNA, complete cds.”//0//1545bp//96%//AF15  
2961

C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
).//1.5E-136//472aa//49%//Q05481

【 0 8 3 6 】

相同性検索結果データ 1 3 .

全長塩基配列および推定アミノ酸配列に対する相同性検索結果データ

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相  
同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000042

C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, compl  
ete cds.//0//1135bp//100%//AF196304

C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.5  
0E-153//525bp//91%//Z70200

C-HEMBA1000213

C-HEMBA1000243

C-HEMBA1000244

C-HEMBA1000251  
C-HEMBA1000338  
C-HEMBA1000357  
C-HEMBA1000376  
C-HEMBA1000428  
C-HEMBA1000469  
C-HEMBA1000497  
C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)  
).//3.40E-37//674aa//25%//Q05481  
C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865  
C-HEMBA1000575  
C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//  
40%//P23246  
C-HEMBA1000673  
C-HEMBA1000702  
C-HEMBA1000722  
C-HEMBA1000726  
C-HEMBA1000876  
C-HEMBA1000942  
C-HEMBA1000943  
C-HEMBA1000960  
C-HEMBA1000985  
C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P3  
4 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//5  
8%//P06493  
C-HEMBA1001020  
C-HEMBA1001024  
C-HEMBA1001026  
C-HEMBA1001051

C-HEMBA1001060

C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82a  
a//100%//P02461

C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma  
mRNA, complete cds.//2.00E-80//432bp//94%//AF119043

C-HEMBA1001099

C-HEMBA1001121

C-HEMBA1001123

C-HEMBA1001208

C-HEMBA1001213

C-HEMBA1001226

C-HEMBA1001247

C-HEMBA1001299

C-HEMBA1001319

C-HEMBA1001323

C-HEMBA1001327

C-HEMBA1001361

C-HEMBA1001375

C-HEMBA1001377

C-HEMBA1001383

C-HEMBA1001391

C-HEMBA1001411

C-HEMBA1001432

C-HEMBA1001433

C-HEMBA1001435

C-HEMBA1001442

C-HEMBA1001463

C-HEMBA1001515

C-HEMBA1001522

C-HEMBA1001557

C-HEMBA1001566

C-HEMBA1001589

C-HEMBA1001608

C-HEMBA1001636

C-HEMBA1001647

C-HEMBA1001651

C-HEMBA1001658

C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E  
-09//101aa//35%//P54787

C-HEMBA1001712

C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN  
) (OSF-4).//1.10E-38//87aa//96%//P55288

C-HEMBA1001745

C-HEMBA1001750

C-HEMBA1001784

C-HEMBA1001791

C-HEMBA1001803

C-HEMBA1001820

C-HEMBA1001835

C-HEMBA1001888

C-HEMBA1001912

C-HEMBA1001915

C-HEMBA1001918

C-HEMBA1001940

C-HEMBA1001942

C-HEMBA1001964

C-HEMBA1002022

C-HEMBA1002039

C-HEMBA1002100

C-HEMBA1002113

C-HEMBA1002119

C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//5  
1aa//49%//Q14847

C-HEMBA1002160

C-HEMBA1002162

C-HEMBA1002166

C-HEMBA1002185

C-HEMBA1002204

C-HEMBA1002328

C-HEMBA1002337

C-HEMBA1002348

C-HEMBA1002381

C-HEMBA1002486

C-HEMBA1002498

C-HEMBA1002538

C-HEMBA1002552

C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%//AF055993

C-HEMBA1002558

C-HEMBA1002621

C-HEMBA1002629

C-HEMBA1002645

C-HEMBA1002659

C-HEMBA1002661

C-HEMBA1002666

C-HEMBA1002678

C-HEMBA1002679

C-HEMBA1002712

C-HEMBA1002716

C-HEMBA1002742

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%/  
/P06746

C-HEMBA1002748

C-HEMBA1002780

C-HEMBA1002801

C-HEMBA1002826

C-HEMBA1002833

C-HEMBA1002921

C-HEMBA1002934

C-HEMBA1002944

C-HEMBA1002968

C-HEMBA1003034

C-HEMBA1003037

C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID  
LABILE CHAIN PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858

C-HEMBA1003078

C-HEMBA1003083

C-HEMBA1003086

C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-  
273//1253bp//99%//AF155096

C-HEMBA1003133

C-HEMBA1003142

C-HEMBA1003166

C-HEMBA1003197

C-HEMBA1003202

C-HEMBA1003220

C-HEMBA1003229

C-HEMBA1003276

C-HEMBA1003278

C-HEMBA1003328

C-HEMBA1003373

C-HEMBA1003597

C-HEMBA1003598

C-HEMBA1003656

C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%/P34629

C-HEMBA1003733

C-HEMBA1003742

C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%/Q16665

C-HEMBA1003803

C-HEMBA1003854

C-HEMBA1003926

C-HEMBA1003939

C-HEMBA1003987

C-HEMBA1004012

C-HEMBA1004015

C-HEMBA1004193

C-HEMBA1004225

C-HEMBA1004241

C-HEMBA1004267

C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%/AF155103

C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%/P22516

C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494  
C-HEMBA1004396  
C-HEMBA1004405  
C-HEMBA1004433  
C-HEMBA1004538  
C-HEMBA1004542  
C-HEMBA1004573  
C-HEMBA1004577  
C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.  
//0//1612bp//99%//AF193844  
C-HEMBA1004617  
C-HEMBA1004631  
C-HEMBA1004705  
C-HEMBA1004733  
C-HEMBA1004748  
C-HEMBA1004778  
C-HEMBA1004803  
C-HEMBA1004807  
C-HEMBA1004820  
C-HEMBA1004865  
C-HEMBA1004880  
C-HEMBA1004900  
C-HEMBA1004909  
C-HEMBA1004960  
C-HEMBA1004978  
C-HEMBA1004980  
C-HEMBA1004983  
C-HEMBA1004995  
C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0/



/2212bp//99%//AB014548

C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487  
bp//99%//AF132947

C-HEMBA1005035

C-HEMBA1005039

C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//  
98%//P35290

C-HEMBA1005050

C-HEMBA1005062

C-HEMBA1005066

C-HEMBA1005075

C-HEMBA1005079

C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete  
cds.//0//2762bp//99%//AF080561

C-HEMBA1005123

C-HEMBA1005149

C-HEMBA1005152

C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608  
bp//99%//AF132941

C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90  
E-179//361aa//95%//Q00004

C-HEMBA1005223

C-HEMBA1005232

C-HEMBA1005241

C-HEMBA1005275

C-HEMBA1005293

C-HEMBA1005311

C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1  
095bp//99%//AJ007581

C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%/P52743  
C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9  
.00E-77//620bp//74%/AF071787  
C-HEMBA1005374  
C-HEMBA1005382  
C-HEMBA1005411  
C-HEMBA1005426  
C-HEMBA1005443  
C-HEMBA1005447  
C-HEMBA1005497  
C-HEMBA1005500  
C-HEMBA1005506  
C-HEMBA1005508  
C-HEMBA1005526  
C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7)  
mRNA, complete cds.//0//1578bp//98%/AF191340  
C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper t  
ranscription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//  
AF134157  
C-HEMBA1005552  
C-HEMBA1005568  
C-HEMBA1005588  
C-HEMBA1005593  
C-HEMBA1005606  
C-HEMBA1005616  
C-HEMBA1005627  
C-HEMBA1005670  
C-HEMBA1005679  
C-HEMBA1005699

C-HEMBA1005705

C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//  
317bp//98%//D14697

C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCI  
UM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//  
33%//P00789

C-HEMBA1005852

C-HEMBA1005894

C-HEMBA1005921

C-HEMBA1006035

C-HEMBA1006036

C-HEMBA1006090

C-HEMBA1006138

C-HEMBA1006173

C-HEMBA1006252

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845  
bp//92%//AF073836

C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-1  
30//332aa//62%//002193

C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//  
381aa//54%//P28160

C-HEMBA1006380

C-HEMBA1006416

C-HEMBA1006421

C-HEMBA1006424

C-HEMBA1006426

C-HEMBA1006446

C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA)./  
/1.90E-81//153aa//97%//P55786

C-HEMBA1006486  
C-HEMBA1006494  
C-HEMBA1006546  
C-HEMBA1006562  
C-HEMBA1006595  
C-HEMBA1006597  
C-HEMBA1006631  
C-HEMBA1006639  
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148  
C-HEMBA1006659  
C-HEMBA1006665  
C-HEMBA1006676  
C-HEMBA1006695  
C-HEMBA1006709  
C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%//AF152492  
C-HEMBA1006780  
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ00644  
C-HEMBA1006824  
C-HEMBA1006865  
C-HEMBA1006921  
C-HEMBA1006949  
C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//447bp//89%//X74570  
C-HEMBA1007051  
C-HEMBA1007052  
C-HEMBA1007066  
C-HEMBA1007073

C-HEMBA1007078

C-HEMBA1007085

C-HEMBA1007113

C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete  
cds.//1.70E-252//1118bp//92%//AF125042.

C-HEMBA1007129

C-HEMBA1007147

C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp/  
/99%//AF076929

C-HEMBA1007178

C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0  
//1212bp//98%//D86987

C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, compl  
ete cds.//0//1590bp//99%//AF196304

C-HEMBA1007243//Chinese hamster hpert mRNA, complete cds.//2.00E-58//650b  
p//70%//J00060

C-HEMBA1007251

C-HEMBA1007288

C-HEMBA1007322

C-HEMBA1007341

C-HEMBA1000050

C-HEMBA1000054

C-HEMBA1000059

C-HEMBA1000089

C-HEMBA1000113

C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL  
GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

C-HEMBA1000173

C-HEMBA1000175

C-HEMBB1000272

C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P  
37888

C-HEMBB1000318

C-HEMBB1000336

C-HEMBB1000341

C-HEMBB1000343

C-HEMBB1000354

C-HEMBB1000374

C-HEMBB1000434

C-HEMBB1000441

C-HEMBB1000491

C-HEMBB1000493

C-HEMBB1000510

C-HEMBB1000652

C-HEMBB1000672

C-HEMBB1000684

C-HEMBB1000709

C-HEMBB1000726

C-HEMBB1000770

C-HEMBB1000827

C-HEMBB1000831

C-HEMBB1000883

C-HEMBB1000888

C-HEMBB1000893

C-HEMBB1000913

C-HEMBB1000996

C-HEMBB1001004

C-HEMBB1001047

C-HEMBB1001060

C-HEMBB1001114

C-HEMBB1001119

C-HEMBB1001133

C-HEMBB1001142

C-HEMBB1001177

C-HEMBB1001208

C-HEMBB1001209

C-HEMBB1001249

C-HEMBB1001253

C-HEMBB1001254

C-HEMBB1001271

C-HEMBB1001304

C-HEMBB1001317

C-HEMBB1001348

C-HEMBB1001394

C-HEMBB1001410

C-HEMBB1001424

C-HEMBB1001426

C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds./

/0//1933bp//99%//AF061738

C-HEMBB1001436

C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase iso

enzyme 1 mRNA, complete cds.//3.00E-130//553bp//86%//AF062740

C-HEMBB1001449

C-HEMBB1001458

C-HEMBB1001521

C-HEMBB1001531

C-HEMBB1001535

C-HEMBB1001536  
C-HEMBB1001564  
C-HEMBB1001565  
C-HEMBB1001585  
C-HEMBB1001588  
C-HEMBB1001603  
C-HEMBB1001618  
C-HEMBB1001635  
C-HEMBB1001653  
C-HEMBB1001668  
C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0  
//2035bp//99%//AB014546  
C-HEMBB1001685  
C-HEMBB1001695  
C-HEMBB1001707  
C-HEMBB1001735  
C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EI  
F3 P116) (EIF3 P110).//4.60E-15//391aa//25%//P55884  
C-HEMBB1001747  
C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q0  
3330  
C-HEMBB1001753  
C-HEMBB1001756  
C-HEMBB1001760  
C-HEMBB1001785  
C-HEMBB1001797  
C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167  
C-HEMBB1001816  
C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI



P1) mRNA, complete cds.//0//1514bp//99%//AF056209  
C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90  
E-11//87aa//35%//P18720  
C-HEMBB1001850  
C-HEMBB1001863  
C-HEMBB1001868  
C-HEMBB1001874  
C-HEMBB1001880  
C-HEMBB1001899  
C-HEMBB1001906  
C-HEMBB1001910  
C-HEMBB1001911  
C-HEMBB1001921  
C-HEMBB1001922  
C-HEMBB1001930  
C-HEMBB1001944  
C-HEMBB1001945  
C-HEMBB1001947  
C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDA  
SE (EC 1.-.-.) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//3  
70aa//31%//P54304  
C-HEMBB1001952  
C-HEMBB1001957  
C-HEMBB1001962  
C-HEMBB1001983  
C-HEMBB1001990  
C-HEMBB1001996  
C-HEMBB1002002  
C-HEMBB1002005

C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49/  
/139aa//55%/P29981

C-HEMBB1002043

C-HEMBB1002045

C-HEMBB1002049

C-HEMBB1002050

C-HEMBB1002068

C-HEMBB1002092

C-HEMBB1002139

C-HEMBB1002142

C-HEMBB1002190

C-HEMBB1002193

C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
).//2.10E-132//399aa//44%/Q05481

C-HEMBB1002218

C-HEMBB1002232

C-HEMBB1002247

C-HEMBB1002249

C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%/P41737

C-HEMBB1002327

C-HEMBB1002329

C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.  
//1.10E-274//1249bp//99%/AJ010841

C-HEMBB1002358

C-HEMBB1002371

C-HEMBB1002387

C-HEMBB1002409

C-HEMBB1002425

C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%/P34692

C-HEMBB1002453

C-HEMBB1002458

C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70

E-258//774bp//99%//U43885

C-HEMBB1002489

C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365

C-HEMBB1002520

C-HEMBB1002522

C-HEMBB1002545

C-HEMBB1002579

C-HEMBB1002582

C-HEMBB1002596

C-HEMBB1002603

C-HEMBB1002610

C-HEMBB1002613

C-HEMBB1002617

C-HEMBB1002623

C-HEMBB1002635

C-HEMBB1002677

C-HEMBB1002683

C-HEMBB1002699

C-HEMBB1002702

C-MAMMA1000009

C-MAMMA1000043

C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRAN  
E PROTEIN GP37] .//1.90E-07//249aa//27%//P03396

C-MAMMA1000057

C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.1  
6) (CYSTEINE-- TRNA LIGASE) (CYSRS) .//2.10E-90//427aa//39%//Q09860

C-MAMMA1000092  
C-MAMMA1000103  
C-MAMMA1000117  
C-MAMMA1000129  
C-MAMMA1000133  
C-MAMMA1000155  
C-MAMMA1000175  
C-MAMMA1000198  
C-MAMMA1000241  
C-MAMMA1000251  
C-MAMMA1000254  
C-MAMMA1000287  
C-MAMMA1000307  
C-MAMMA1000331  
C-MAMMA1000339  
C-MAMMA1000340  
C-MAMMA1000348  
C-MAMMA1000356  
C-MAMMA1000360  
C-MAMMA1000402  
C-MAMMA1000414  
C-MAMMA1000431  
C-MAMMA1000444  
C-MAMMA1000458  
C-MAMMA1000500  
C-MAMMA1000522  
C-MAMMA1000576  
C-MAMMA1000583  
C-MAMMA1000594

C-MAMMA1000605

C-MAMMA1000616

C-MAMMA1000643

C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//A  
F109134

C-MAMMA1000696

C-MAMMA1000707

C-MAMMA1000714

C-MAMMA1000720

C-MAMMA1000744

C-MAMMA1000761

C-MAMMA1000776

C-MAMMA1000798

C-MAMMA1000839

C-MAMMA1000851

C-MAMMA1000863

C-MAMMA1000867

C-MAMMA1000876

C-MAMMA1000880

C-MAMMA1000883

C-MAMMA1000921

C-MAMMA1000931

C-MAMMA1000941

C-MAMMA1000957

C-MAMMA1000962

C-MAMMA1000975

C-MAMMA1000987

C-MAMMA1001003

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (

LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%  
//Q90674

C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE  
ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//9  
5%//Q15746

C-MAMMA1001082

C-MAMMA1001162

C-MAMMA1001186

C-MAMMA1001191

C-MAMMA1001206

C-MAMMA1001220

C-MAMMA1001243

C-MAMMA1001249

C-MAMMA1001256

C-MAMMA1001268

C-MAMMA1001271

C-MAMMA1001274

C-MAMMA1001292

C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN  
IN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-AC  
TIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960

C-MAMMA1001324

C-MAMMA1001341

C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312  
aa//99%//P02750

C-MAMMA1001397

C-MAMMA1001408

C-MAMMA1001420

C-MAMMA1001442

C-MAMMA1001452

C-MAMMA1001465

C-MAMMA1001487

C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

C-MAMMA1001547

C-MAMMA1001551

C-MAMMA1001575

C-MAMMA1001590

C-MAMMA1001600

C-MAMMA1001606

C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989

C-MAMMA1001663

C-MAMMA1001670

C-MAMMA1001671

C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756

C-MAMMA1001711

C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653

C-MAMMA1001744

C-MAMMA1001745

C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708

C-MAMMA1001783

C-MAMMA1001788

C-MAMMA1001806

C-MAMMA1001812  
C-MAMMA1001815  
C-MAMMA1001817  
C-MAMMA1001818  
C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157  
bp//80%//Y13148  
C-MAMMA1001824  
C-MAMMA1001851  
C-MAMMA1001854  
C-MAMMA1001864  
C-MAMMA1001878  
C-MAMMA1001890  
C-MAMMA1001907  
C-MAMMA1001908  
C-MAMMA1001931  
C-MAMMA1001969  
C-MAMMA1002011  
C-MAMMA1002032  
C-MAMMA1002041  
C-MAMMA1002047  
C-MAMMA1002056  
C-MAMMA1002058  
C-MAMMA1002078  
C-MAMMA1002082  
C-MAMMA1002084  
C-MAMMA1002093  
C-MAMMA1002094  
C-MAMMA1002118  
C-MAMMA1002125



C-MAMMA1002132

C-MAMMA1002140

C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds  
./1.70E-252//1170bp//99%//AF099664

C-MAMMA1002145

C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE  
REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL  
KILLER CELL ENHANCING FACTOR B) (NKEF-B)./5.20E-61//60aa//90%//P32119

C-MAMMA1002230

C-MAMMA1002250

C-MAMMA1002282

C-MAMMA1002293

C-MAMMA1002298

C-MAMMA1002299

C-MAMMA1002308

C-MAMMA1002310

C-MAMMA1002311

C-MAMMA1002322

C-MAMMA1002339

C-MAMMA1002352

C-MAMMA1002359

C-MAMMA1002360

C-MAMMA1002392

C-MAMMA1002411

C-MAMMA1002413

C-MAMMA1002417

C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL  
MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2)./1.10E-24//96  
aa//68%//Q14108

C-MAMMA1002434  
C-MAMMA1002446  
C-MAMMA1002454  
C-MAMMA1002461  
C-MAMMA1002475  
C-MAMMA1002556  
C-MAMMA1002566  
C-MAMMA1002612  
C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q0786  
6  
C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-5  
7//480bp//68%//AF194030  
C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA,  
complete cds.//4.3e-317//1942bp//85%//AF018261  
C-MAMMA1002727  
C-MAMMA1002748  
C-MAMMA1002758  
C-MAMMA1002780  
C-MAMMA1002820  
C-MAMMA1002833  
C-MAMMA1002843  
C-MAMMA1002895  
C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742  
C-MAMMA1003004  
C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein  
PIASy mRNA, complete cds.//0//1533bp//99%//AF077952  
C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X801

C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886

C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590

C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561

C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775

C-NT2RM1000499

C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//Q99383

C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481

C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990

C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518

C-NT2RM2001637

C-NT2RM2001641

C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230

C-NT2RM2001699

C-NT2RM2001706

C-NT2RM2001718

C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931

C-NT2RM2001805

C-NT2RM4000086

C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962

C-NT2RM4000414

C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28  
%//Q04652

C-NT2RM4000634

C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0/  
/1412bp//100%//AB028992

C-NT2RM4000783

C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250a  
a//29%//P02750

C-NT2RM4000971

C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
).//8.00E-211//738aa//50%//Q05481

C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%//P38682

C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218  
aa//43%//Q03532

C-NT2RM4001569

C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein  
kinase) mRNA, complete cds.//8.10E-300//1395bp//98%//M37712

C-NT2RM4001905

C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0/  
/2234bp//99%//AB020705

C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA  
LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419

C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partia  
l cds.//9.30E-293//1751bp//83%//AF072758

C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein  
(PTB) mRNA, complete cds.//0//2550bp//99%//AF176085

C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, comple  
te cds.//0//2572bp//99%//AF071592

C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp/

/85%//AF035940

C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-2

97//1753bp//87%//AF030430

C-NT2RM4002390

C-NT2RM4002398

C-NT2RM4002420

C-NT2RM4002534

C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962

C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%//X85019

C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//88%//AL050019

C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//8.20E-83//345aa//47%//Q61068

C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//99%//AL050118

C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721

C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//1687bp//99%//AF145020

C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020

C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094

C-NT2RP1000916

C-NT2RP1000944

C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, comp

lete cds.//0//2085bp//99%//U82267

C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//31  
9aa//46%//Q06218

C-NT2RP1001113

C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp5  
66D1146).//0//2333bp//99%//AL080222

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds  
./5.20E-108//1278bp//69%//U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete  
cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LE  
FTYA mRNA, complete cds.//0//2006bp//100%//AF081513

C-NT2RP1001311

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complet  
e cds.//7.50E-121//1394bp//69%//AF126799

C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0/  
/3188bp//99%//AB029034

C-NT2RP2000027

C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SP  
ECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//002675

C-NT2RP2000198

C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).  
//6.00E-16//124aa//34%//P41238

C-NT2RP2000551

C-NT2RP2000644

C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

C-NT2RP2000678

C-NT2RP2000715

C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, compl

ete cds.//0//1562bp//99%/U80811

C-NT2RP2000970

C-NT2RP2001347

C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%/P37709

C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%/P24391

C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%/U97067

C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%/AF058718

C-NT2RP2001677

C-NT2RP2001678

C-NT2RP2001720

C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%/Q61068

C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%/P51523

C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%/P53009

C-NT2RP2001861

C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%/O14754

C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%/P55008

C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%/M74161

C-NT2RP2001936

C-NT2RP2001943

C-NT2RP2001946  
C-NT2RP2002032  
C-NT2RP2002033  
C-NT2RP2002041  
C-NT2RP2002047  
C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306  
C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0/  
/1772bp//95%//AB029020  
C-NT2RP2002172  
C-NT2RP2002219  
C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418  
C-NT2RP2002316  
C-NT2RP2002373  
C-NT2RP2002439  
C-NT2RP2002475  
C-NT2RP2002546  
C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20  
E-155//562aa//50%//P51523  
C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147/  
/874bp//87%//U19181  
C-NT2RP2002643  
C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74/  
/727bp//72%//AF041107  
C-NT2RP2002736  
C-NT2RP2002740  
C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90  
E-54//964bp//64%//D89016



C-NT2RP2002752

C-NT2RP2002753

C-NT2RP2002857

C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.90E-11//132aa//38%//Q13829

C-NT2RP2003073

C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545

C-NT2RP2003206

C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794

C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657

C-NT2RP2003237

C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069

C-NT2RP2003280

C-NT2RP2003293

C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//5.50E-13//302aa//26%//P25386

C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//Q61068

C-NT2RP2003456

C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783

C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158

C-NT2RP2003559

C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)

) (RO(SS-A)).//2.10E-59//270aa//46%/P19474  
C-NT2RP2003581  
C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%/AJ006215  
C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type V II (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%/AF098786  
C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1 L.//1.80E-72//350bp//100%/AJ132637  
C-NT2RP2003727  
C-NT2RP2003751  
C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%/Q09201  
C-NT2RP2003825  
C-NT2RP2003871  
C-NT2RP2003885  
C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%/P51954  
C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0.2866kb//98%/AB007916  
C-NT2RP2003988  
C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//2.30E-53//141aa//78%/P20290  
C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%/Q01513  
C-NT2RP2004142  
C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%/Y12781  
C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%/AF003998

C-NT2RP2004207

C-NT2RP2004226

C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//AB015982

C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//9.90E-12//427aa//26%//P19246

C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857

C-NT2RP2004321

C-NT2RP2004339

C-NT2RP2004347

C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//99%//AB028069

C-NT2RP2004399

C-NT2RP2004400

C-NT2RP2004412

C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739

C-NT2RP2004490

C-NT2RP2004523

C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//AF090190

C-NT2RP2004580

C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%//AB020695

C-NT2RP2004594

C-NT2RP2004681

C-NT2RP2004709

C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%//AB023231

C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0/  
/1774bp//99%//AB020691  
C-NT2RP2004767  
C-NT2RP2004775  
C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1  
(KS1) mRNA, complete cds.//1.00E-228//1666bp//75%//U56732  
C-NT2RP2004962  
C-NT2RP2004982  
C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//1.80E-99//376aa//43%//P19474  
C-NT2RP2005018  
C-NT2RP2005020  
C-NT2RP2005022  
C-NT2RP2005031  
C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//0/  
/4069bp//99%//AB014564  
C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDEN  
T RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35  
%//Q05921  
C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//  
2769bp//98%//AJ007509  
C-NT2RP2005254  
C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA,  
complete cds.//0//1643bp//99%//AF124735  
C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709  
C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2  
.10E-124//636aa//38%//P32660  
C-NT2RP2005360  
C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059

C-NT2RP2005454

C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.  
5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652

C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//66  
8bp//88%//U17032

C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P  
35418

C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742

C-NT2RP2005501

C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P1  
1171

C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0/  
/2554bp//99%//AB028943

C-NT2RP2005645

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-1  
0//175aa//27%//Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63/  
/323aa//39%//Q62158

C-NT2RP2005741

C-NT2RP2005806

C-NT2RP2005815

C-NT2RP2005841

C-NT2RP2005882

C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A  
DENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500

C-NT2RP2006103

C-NT2RP2006166

C-NT2RP2006258

C-NT2RP2006261

C-NT2RP2006321

C-NT2RP2006454

C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA  
A, complete cds.//3.10E-295//1193bp//99%//AF113538

C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//3  
7%//P32559

C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755

C-NT2RP3000418

C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGI  
ON.//2.90E-15//319aa//26%//P37908

C-NT2RP3000487

C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X  
16667

C-NT2RP3000526

C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42  
%//Q13562

C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82  
%//AB012265

C-NT2RP3000628

C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN  
) .//1.40E-24//155aa//37%//Q10149

C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-  
) .//8.30E-108//331aa//50%//P27448

C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027

C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
) .//9.00E-201//584aa//54%//Q05481

C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//2.90E-11/  
/631aa//23%//P25386

C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0

//2659bp//99%//AB023140

C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)./  
/1.70E-10//540aa//23%//P32380

C-NT2RP3001356

C-NT2RP3001383

C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538

C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN  
LC1] .//1.40E-76//388aa//32%//P46821

C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//17  
88bp//99%//AF113534

C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein m  
RNA, complete cds.//1.10E-240//902bp//99%//AF054177

C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)  
mRNA, partial cds.//6.90E-132//774bp//88%//AF008554

C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14  
141

C-NT2RP3001739

C-NT2RP3001777

C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//  
242aa//24%//Q00808

C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0  
//3747bp//99%//AB014575

C-NT2RP3001944

C-NT2RP3002033

C-NT2RP3002054

C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0/  
/2830bp//99%//AB028956

C-NT2RP3002099

C-NT2RP3002102

C-NT2RP3002147

C-NT2RP3002163

C-NT2RP3002173

C-NT2RP3002255

C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767

C-NT2RP3002343

C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396

C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991

C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578

C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//99%//AL050092

C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III./5.80E-40//161aa//52%//Q10010

C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598

C-NT2RP3002603

C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660

C-NT2RP3002659

C-NT2RP3002660

C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903



C-NT2RP3002687

C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.10E-93//1205bp//69%//D17577

C-NT2RP3002701

C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55  
//187aa//39%//Q24371

C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-2  
32//1282bp//85%//AF030430

C-NT2RP3002876

C-NT2RP3002877

C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0/  
/2085bp//94%//AB018314

C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053

C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.9  
0E-52//899bp//64%//AB029333

C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%//AF084555

C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357

C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23  
645

C-NT2RP3003078

C-NT2RP3003139

C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF077738

C-NT2RP3003150

C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//  
5.70E-09//169aa//31%//Q09674

C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55

mRNA, complete cds.//2.00E-210//1851bp//76%//AF110267  
C-NT2RP3003210  
C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1  
C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286  
C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//  
99%//AB030656  
C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complet  
e cds.//0//2366bp//99%//AF098462  
C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//4.20E-86//366aa//48%//P19474  
C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.2  
1.-).//1.10E-170//585aa//54%//064948  
C-NT2RP3003311  
C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA,  
complete cds.//9.20E-45//782bp//65%//U90653  
C-NT2RP3003427  
C-NT2RP3003543  
C-NT2RP3003552  
C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC RE  
GION.//4.50E-30//191aa//40%//P40529  
C-NT2RP3003564  
C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, compl  
ete cds.//0//3131bp//94%//AF106681  
C-NT2RP3003621  
C-NT2RP3003625  
C-NT2RP3003656  
C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843  
C-NT2RP3003686  
C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446

C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%/P24014  
C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%/U28164  
C-NT2RP3003795  
C-NT2RP3003805  
C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%/Q07590  
C-NT2RP3003819  
C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19/  
/174aa//31%/P02720  
C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%/AB020523  
C-NT2RP3003833  
C-NT2RP3003842  
C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%/AB019435  
C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%/AB018343  
C-NT2RP3003876  
C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%/Q09332  
C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%/AF086628  
C-NT2RP3003989  
C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%/Q13263  
C-NT2RP3004070  
C-NT2RP3004145  
C-NT2RP3004215  
C-NT2RP3004253

C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871

C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//X67877

C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence .//0//1778bp//99%//AC003982

C-NT2RP3004503

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523

C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679

C-NT2RP4000023

C-NT2RP4000218

C-NT2RP4000424

C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676

C-NT2RP4001447

C-NT2RP4001841

C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194

C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618

C-NT2RP4002075

C-NT2RP4002083

C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290

C-OVARC1000008

C-OVARC1000017

C-OVARC1000058

C-OVARC1000068

C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA

A, complete cds.//1.50E-47//727bp//67%//AF156957  
C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp  
//100%//D00761  
C-OVARC1000109  
C-OVARC1000114  
C-OVARC1000145  
C-OVARC1000240  
C-OVARC1000302  
C-OVARC1000408  
C-OVARC1000414  
C-OVARC1000440  
C-OVARC1000442  
C-OVARC1000496  
C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6K  
II-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30  
E-67//132aa//95%//Q15349  
C-OVARC1000557  
C-OVARC1000578  
C-OVARC1000622  
C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//9  
9%//AF117888  
C-OVARC1000681  
C-OVARC1000700  
C-OVARC1000724  
C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (  
PP2C).//5.60E-11//74aa//37%//P49596  
C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE  
REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501  
C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%/

/P37440

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa/  
/28%/P03398

C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aaaa//49%/P32943

C-OVARC1000960

C-OVARC1000971

C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%/Q06527

C-OVARC1001000

C-OVARC1001029

C-OVARC1001040

C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15  
(PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%/P42566

C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5  
.1e-310//1588bp//93%/AF051782

C-OVARC1001118

C-OVARC1001129

C-OVARC1001169

C-OVARC1001240

C-OVARC1001261

C-OVARC1001339

C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%/P09058

C-OVARC1001357

C-OVARC1001442

C-OVARC1001611

C-OVARC1001813

C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//0/  
/1760bp//99%/AF054174

C-OVARC1002143

C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (S

TEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%/P31213  
C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (B  
TRCP).//1.70E-09//207aa//30%/Q91854  
C-PLACE1000014  
C-PLACE1000078  
C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, comp  
lete cds.//0//2041bp//87%/U35245  
C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%/P23  
645  
C-PLACE1000814  
C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%/P52742  
C-PLACE1001007  
C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, com  
plete cds.//4.00E-300//1355bp//100%/AB024301  
C-PLACE1001088  
C-PLACE1001136  
C-PLACE1001241  
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-  
228//827bp//99%/AF009615  
C-PLACE1001395  
C-PLACE1001740  
C-PLACE1001746  
C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGI  
ON.//7.50E-16//319aa//26%/P37908  
C-PLACE1002066  
C-PLACE1002115  
C-PLACE1002213  
C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//0/  
/1657bp//98%/AB018271

C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp  
//99%//U69274

C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0  
//2092bp//84%//U69262

C-PLACE1002499

C-PLACE1002578

C-PLACE1002714

C-PLACE1002772

C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201

C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50  
E-203//396aa//86%//P51522

C-PLACE1002993

C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subu  
nit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387

C-PLACE1003205

C-PLACE1003249

C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//594aa/  
/33%//P28481

C-PLACE1003553

C-PLACE1003592

C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-  
93//270aa//66%//P46975

C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793

C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA,  
complete cds.//6.20E-282//1316bp//98%//AF053305

C-PLACE1003870

C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE A  
DENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500

C-PLACE1003892



C-PLACE1003900  
C-PLACE1004336  
C-PLACE1004384  
C-PLACE1004425  
C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90  
E-56//276aa//41%//P51522  
C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1  
) mRNA, complete cds.//2.10E-16//402bp//62%//U90878  
C-PLACE1004518  
C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-2  
74//1305bp//97%//AF132954  
C-PLACE1004681  
C-PLACE1004693  
C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-  
103//586bp//91%//AF125099  
C-PLACE1004815  
C-PLACE1004836  
C-PLACE1004838  
C-PLACE1004840  
C-PLACE1004900  
C-PLACE1004985  
C-PLACE1005085  
C-PLACE1005086  
C-PLACE1005108  
C-PLACE1005146  
C-PLACE1005409  
C-PLACE1005453  
C-PLACE1005477  
C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288

C-PLACE1005595

C-PLACE1005603

C-PLACE1005639

C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//  
2.00E-118//378bp//98%//AF162680

C-PLACE1005799

C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./  
/0//2040bp//99%//AF065482

C-PLACE1005884

C-PLACE1005968

C-PLACE1006002

C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-1  
77//829bp//99%//AF151852

C-PLACE1006017

C-PLACE1006037

C-PLACE1006076

C-PLACE1006143

C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0/  
/1489bp//100%//AB014548

C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDA  
C1) (PLASMALEMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (P  
ORIN 31HL) (PORIN 31HM).//4.60E-117//147aa//80%//P21796

C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-0  
7//376bp//59%//U76374

C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID R  
ECEPTOR).//1.30E-18//460aa//24%//Q00547

C-PLACE1006371

C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA  
LIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%//P27550

C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4)  
mRNA, complete cds.//0//2170bp//99%//AF191338

C-PLACE1006521

C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp5  
64G1964).//1.70E-192//883bp//99%//AL110144

C-PLACE1006617

C-PLACE1006640

C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66)  
(CD66A ANTIGEN).//6.20E-63//191aa//43%//P13688

C-PLACE1006760

C-PLACE1006779

C-PLACE1006805

C-PLACE1006815

C-PLACE1006867

C-PLACE1007045

C-PLACE1007097

C-PLACE1007111

C-PLACE1007112

C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0  
//3492bp//99%//AB023226

C-PLACE1007218

C-PLACE1007454

C-PLACE1007478

C-PLACE1007677

C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complet  
e cds.//1.10E-184//1096bp//82%//AB033922

C-PLACE1007737

C-PLACE1007743

C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1

.00E-232//1174bp//94%//AB020685

C-PLACE1007877

C-PLACE1008045

C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//  
2152bp//99%//AB021179

C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//  
37%//Q03326

C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//226  
5bp//83%//L23077

C-PLACE1008231

C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//  
148aa//38%//Q00808

C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDE  
N CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.  
20E-23//94aa//47%//Q05315

C-PLACE1008331

C-PLACE1008369

C-PLACE1008392

C-PLACE1008405

C-PLACE1008424

C-PLACE1008584

C-PLACE1008625

C-PLACE1008630

C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (  
ITI HEAVY CHAIN H2).//5.20E-90//483aa//38%//002668

C-PLACE1008715

C-PLACE1008748

C-PLACE1008757

C-PLACE1008798

C-PLACE1008851  
C-PLACE1008947  
C-PLACE1009039  
C-PLACE1009048  
C-PLACE1009050  
C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3  
(XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586  
C-PLACE1009150  
C-PLACE1009200  
C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P2967  
5  
C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, c  
omplete cds.//0//2262bp//99%//AF191298  
C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//2  
3%//P14922  
C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742  
C-PLACE1009410  
C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.  
50E-148//592bp//99%//AB014584  
C-PLACE1009493  
C-PLACE1009539  
C-PLACE1009595  
C-PLACE1009637  
C-PLACE1009639  
C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552  
C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4  
.22.-).//6.50E-28//209aa//38%//P43510  
C-PLACE1009888  
C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0

//1730bp//99%//AF038963

C-PLACE1009947

C-PLACE1010069

C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0/  
/1554bp//100%//AB029020

C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE R  
ECEPTOR).//5.10E-27//371aa//28%//Q14246

C-PLACE1010270

C-PLACE1010562

C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, comp  
lete cds.//9.30E-299//1362bp//99%//AF200715

C-PLACE1010624

C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypohethica  
l protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//32  
4bp//64%//AF109907

C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (   
EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332

C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//  
427aa//55%//P28160

C-PLACE1010761

C-PLACE1010802

C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209

C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)./  
/1.50E-25//583aa//23%//P35580

C-PLACE1010916

C-PLACE1010947

C-PLACE1010965

C-PLACE1011032

C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds./

/0//1701bp//97%//AB015019  
 C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256  
 C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//99%//AL050159  
 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663  
 C-PLACE1011214  
 C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604  
 C-PLACE1011273  
 C-PLACE1011291  
 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587  
 C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703  
 C-PLACE1011503  
 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377  
 C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752  
 C-PLACE1011650  
 C-PLACE1011675  
 C-PLACE1011725  
 C-PLACE1011749  
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580  
 C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256  
 C-PLACE2000006

C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0/  
/1968bp//97%//AB020720

C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.  
1.3.48).//2.20E-29//212aa//35%//P10586

C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C  
) , mRNA, complete cds.//4.60E-291//1167bp//89%//L08505

C-PLACE2000061

C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0  
//3174bp//99%//AF027219

C-PLACE2000097

C-PLACE2000103

C-PLACE2000115

C-PLACE2000124

C-PLACE2000140

C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736

C-PLACE2000176

C-PLACE2000223

C-PLACE2000235

C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P230  
98

C-PLACE2000302

C-PLACE2000347

C-PLACE2000359

C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205

C-PLACE2000379

C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (C  
D99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209

C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--T  
RNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996



C-PLACE2000450

C-PLACE2000455

C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//  
1979bp//90%//Y17267

C-PLACE3000070

C-PLACE3000119

C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281a  
a//22%//P22224

C-PLACE3000136

C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type  
1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084

C-PLACE3000148

C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2  
.10E-75//382bp//99%//AB014572

C-PLACE3000160

C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742

C-PLACE3000194

C-PLACE3000199

C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POM  
T2) mRNA, complete cds.//0//1862bp//98%//AF105020

C-PLACE3000230

C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435a  
a//92%//P53995

C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRN  
A, complete cds.//0//4583bp//83%//AF143946

C-PLACE3000276

C-PLACE3000310

C-PLACE3000320

C-PLACE3000331

C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa/  
/23%//P08640

C-PLACE3000352

C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp5  
86H0623).//0//2456bp//99%//AL096739

C-PLACE3000362

C-PLACE3000365

C-PLACE3000388

C-PLACE3000413

C-PLACE3000425

C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HE  
AVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580

C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//  
3.10E-111//348aa//41%//P46100

C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) m  
RNA, complete cds.//0//4661bp//99%//AF165281

C-PLACE4000089

C-PLACE4000128//Mus musculus putative transcription factor mRNA, complet  
e cds.//1.60E-86//190aa//88%//AF091234

C-PLACE4000129

C-PLACE4000147

C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//  
369aa//25%//P52746

C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial c  
ds.//1.70E-262//1217bp//98%//AF000422

C-PLACE4000222

C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0/  
/3787bp//99%//AB028990

C-PLACE4000270  
 C-PLACE4000300  
 C-PLACE4000387  
 C-PLACE4000392  
 C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//  
 5142bp//90%//Z70200  
 C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial c  
 ds.//2.70E-261//1217bp//98%//AF000422  
 C-PLACE4000465  
 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT  
 I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%  
 //P13002  
 C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//  
 6340bp//87%//Y17267  
 C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUB  
 UNIT).//5.50E-35//431aa//29%//O60100  
 C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162  
 //749bp//99%//AF034800  
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CAL  
 CIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%  
 //P17655  
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709  
 C-THYRO1000070  
 C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE  
 ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29  
 %//P11799  
 C-THYRO1000092  
 C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0  
 //2159bp//99%//AB029039

C-THYRO1000124

C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0/  
/2362bp//99%//AJ005698

C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0  
//1409bp//98%//AB014552

C-THYRO1000206

C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00  
E-118//239aa//66%//P51523

C-THYRO1000253

C-THYRO1000270

C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161b  
p//99%//AB016068

C-THYRO1000320

C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//  
P17563

C-THYRO1000368

C-THYRO1000381

C-THYRO1000387

C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, c  
omplete cds.//1.20E-299//1325bp//99%//AF072864

C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete  
cds.//0//2092bp//99%//AF156857

C-THYRO1000401

C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%/  
/AB022663

C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)  
) (RO(SS-A)).//4.20E-98//408aa//42%//P19474

C-THYRO1000558

C-THYRO1000570

C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360

C-THYRO1000625

C-THYRO1000637

C-THYRO1000676

C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679

C-THYRO1000712

C-THYRO1000805

C-THYRO1000815

C-THYRO1000855

C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%//P32322

C-THYRO1000988

C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948

C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//1479bp//66%//U38252

C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276

C-THYRO1001262

C-THYRO1001271

C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701

C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861

C-THYRO1001347

C-THYRO1001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//99%//AL080120

C-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//0//1700bp//99%//AB014607

C-THYRO1001403

C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427

C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%//AF078850

C-THYRO1001426

C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580

C-THYRO1001480

C-THYRO1001487

C-THYRO1001584

C-THYRO1001661

C-THYRO1001746

C-THYRO1001772

C-THYRO1001854

C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%//AF171060

C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484

C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//AF123534

C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835

C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692

C-Y79AA1000410

C-Y79AA1000539

C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence./  
/1.00E-302//1375bp//99%//AF091080

C-Y79AA1000802

C-Y79AA1000827

C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds./  
/0//1586bp//99%//AF100757

C-Y79AA1000969

C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4  
.70E-151//985bp//87%//U52962

C-Y79AA1001061

C-Y79AA1001068

C-Y79AA1001216

C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (I  
NI1B).//0//996bp//99%//AJ011738

C-Y79AA1001511

C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID R  
ECEPTOR).//2.50E-14//410aa//24%//Q00547

C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl)  
mRNA, complete cds.//1.40E-78//227aa//40%//Q01820

C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, c-  
omplete cds.//0//2927bp//97%//AF192913

C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPT  
IONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//1  
35aa//31%//P43489

C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q  
24133

C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHEL  
IAL (B12 PROTEIN).//0.0000018//140aa//25%//Q13829

C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3  
./1.70E-17//146aa//35%//016264  
C-Y79AA1002220  
C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0/  
/3168bp//99%//AB014592  
C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//9  
9%//AB013384  
C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-sub  
unit).//6.90E-140//966bp//82%//Y18208  
C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X9  
1879  
C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, comple  
te cds.//3.9e-317//1902bp//86%//U49385  
C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//31  
8aa//35%//Q04725  
C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7  
).//2.70E-137//340aa//51%//Q05481  
C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA  
, complete cds.//7.3e-311//1444bp//98%//AF129534

【 0 8 3 7 】

【配列表】

【図面の簡単な説明】

【図 1】 pME18SFL3とpUC19FL3のベクターのマップ

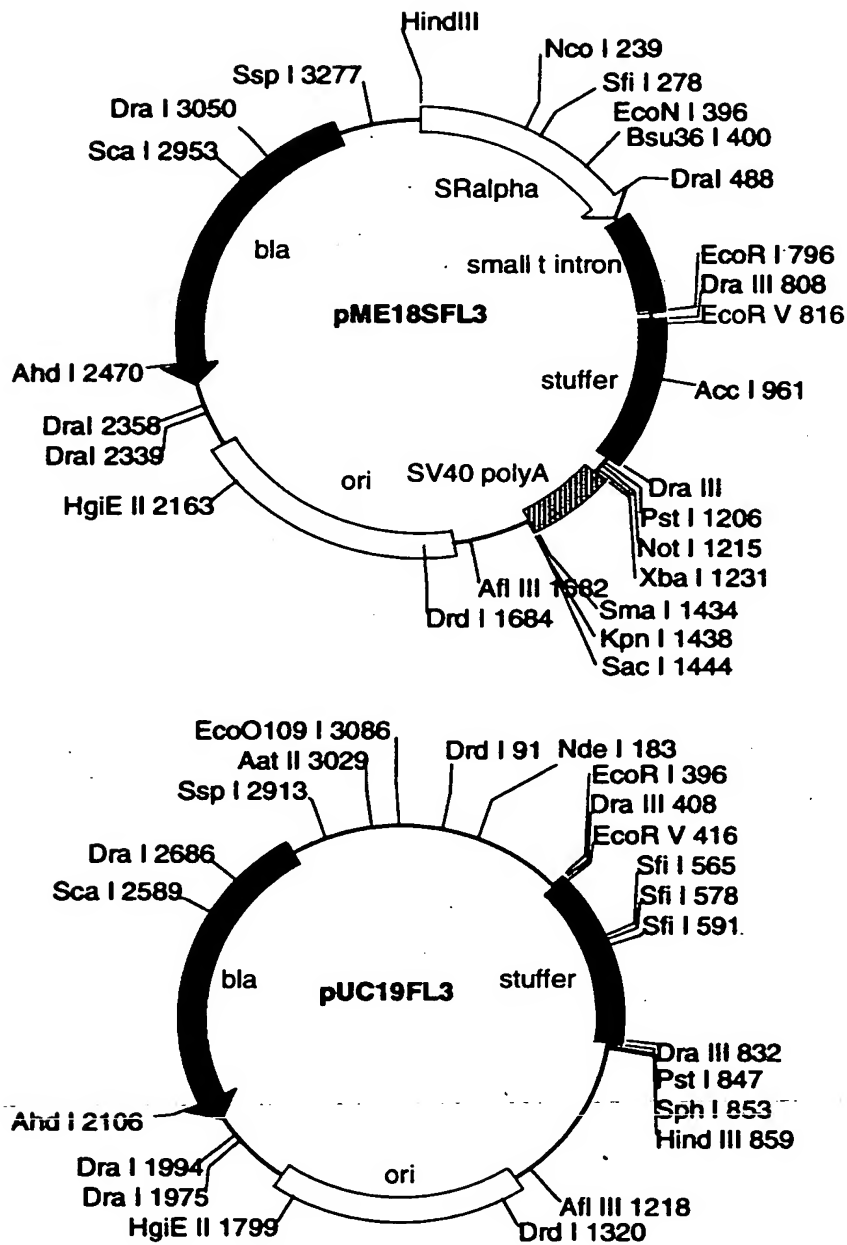
【図 2】 遺伝子発現解析の再現性を示すグラフ。縦軸と横軸はそれぞれ異なる実験によって得られた発現強度を示している。

【図 3】 遺伝子発現解析における検出感度を示すグラフ。縦軸は発現強度を、横軸はプローブの濃度 ( $\mu\text{g/ml}$ ) を示す。

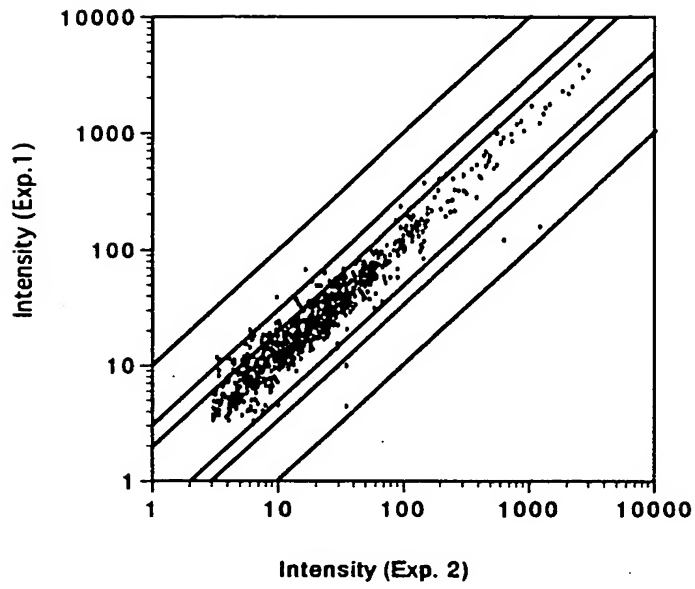


【書類名】 図面

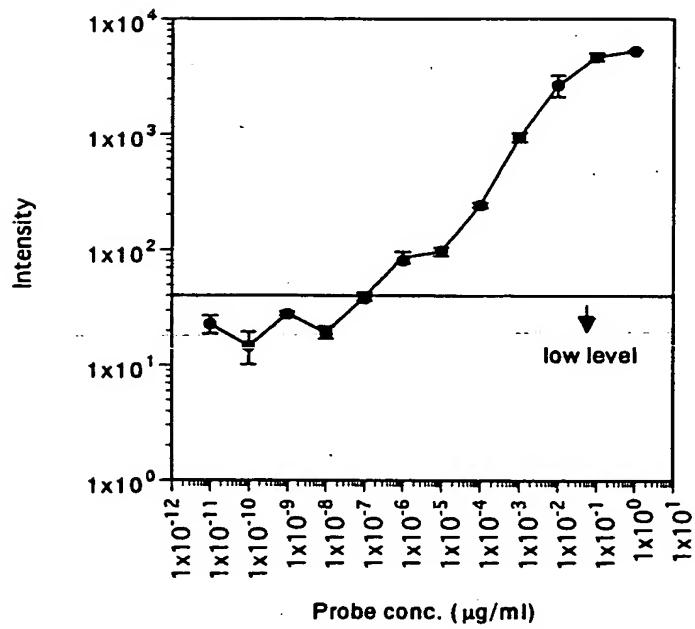
【図 1】



【図 2】



【図 3】



【書類名】 要約書

【要約】

【課題】 全長cDNAを合成することができるプライマーとその用途の提供。

【解決手段】 ヒトのタンパク質をコードする5601のcDNAを単離した。そしてこのcDNAの5'側、および3'側の塩基配列を明らかにした。得られた塩基配列に基づいて、全長cDNA合成用プライマーを提供するとともに、cDNAによってコードされるタンパク質の機能を明らかにした。本発明のcDNAは全長であるため、翻訳開始点を含み、タンパク質の機能解析において有用な情報を与える。

【選択図】 なし

職権訂正履歴（書類修正）

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<修正内容>

- ・「物件電子化フラグ（X083）」：' 2'（物件電子化無し・返還無し）
- ・「提出物件名（X081）」：' CD-R DNA配列表' としてください。

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